



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Takashi OKADO et al.
- (ii) TITLE OF INVENTION: GENE REGULATING AUREOBASIDIN SENSITIVITY
(AS AMENDED)
- (iii) NUMBER OF SEQUENCES: 50
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: WENDEROTH, LIND & PONACK, L.L.P.
 - (B) STREET: 2033 K Street, N.W., #800
 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 20006
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: MS-DOS
 - (D) SOFTWARE: wordperfect 5.1
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 10/777,195
 - (B) FILING DATE: February 13, 2004
- (vii) PRIOR APPLICATION DATA
 - (A) APPLICATION NUMBER: 09/368,431
 - (B) FILING DATE: August 5, 1999
- (viii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/716,873
 - (B) FILING DATE: September 20, 1996
- (ix) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Warren M. Cheek, Jr.
- (B) REGISTRATION NUMBER: 33,367
- (C) REFERENCE/DOCKET NUMBER: 2003-1772/WMC/00001
- (x) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 202-721-8200
 - (B) TELEFAX: 202-721-8250
 - (C) TELEX:
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4140 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Genomic DNA

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cgtctgagac tcgtcagtca gccattcgag tatgcgaact ctgactttgc tcacctaaga  240
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 cctgccagtg agttaaaaac aaccgcgtac cagaccccggt gcagcagtta ctcacatatg 1560
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 gtgggcaaca atgtacctc caccacta tgcggtcgat ttggttgagg gtggtctcct 2160
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 tgctcgcag gtttatccat tcgctcaaag tggattacgt ccacatatta cccgggggct 3240
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 ctattgccac tttgtccata tctcttgctt gtaatagaac tgacatcgcg acgcttcggc 3660
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 caagcagact aaatatttaa cgtgggatat tattcatata cgcatatgta tacatagtca 3840
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 atgcgacgtc agactggaac caggaagga aaggagagag gtacctgtat ttggaccacc 4140

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asn Gln Thr Leu Pro Thr Trp Lys Asp Arg Thr Gln Asn Gln

1	5	10	15
Phe Gly Lys Leu Gln Ile Gln Val Pro Trp Arg Ser Ile Gln Leu			
	20	25	30
Leu Val Pro His Arg Met Arg Arg Lys Leu Arg Ser Lys Leu Arg			
	35	40	45
Ser Arg Ala Ser Pro Thr Ser Ser Ile Ala Ser Leu Gln Thr Ser			
	50	55	60
Leu Ser Pro Ala Asp Thr Leu Arg Ser Leu Gln Ser His Arg Trp			
	65	70	75
Thr Val Tyr Asp Phe Gln Tyr Leu Leu Leu Leu Ile Val Gly Ile			
	80	85	90
Phe Ser Leu Thr Val Ile Glu Ser Pro Gly Pro Leu Gly Lys Thr			
	95	100	105
Ala Ile Phe Ser Met Leu Leu Phe Ser Leu Leu Ile Pro Met Thr			
	110	115	120
Arg Gln Phe Phe Leu Pro Phe Leu Pro Ile Ala Gly Trp Leu Leu			
	125	130	135
Phe Phe Tyr Ala Cys Gln Phe Ile Pro Ser Asp Trp Arg Pro Ala			
	140	145	150
Ile Trp Val Arg Val Leu Pro Ala Leu Glu Asn Ile Leu Tyr Gly			
	155	160	165
Ala Asn Ile Ser Asn Ile Leu Ser Ala His Gln Asn Val Val Leu			
	170	175	180
Asp Val Leu Ala Trp Leu Pro Tyr Gly Ile Cys His Tyr Gly Ala			
	185	190	195
Pro Phe Val Cys Ser Leu Ile Met Phe Ile Phe Gly Pro Pro Gly			
	200	205	210
Thr Val Pro Leu Phe Ala Arg Thr Phe Gly Tyr Ile Ser Met Thr			
	215	220	225
Ala Val Thr Ile Gln Leu Phe Phe Pro Cys Ser Pro Pro Trp Tyr			
	230	235	240
Glu Asn Arg Tyr Gly Leu Ala Pro Ala Asp Tyr Ser Ile Gln Gly			

245	250	255
Asp Pro Ala Gly Leu Ala Arg Ile Asp	Lys Leu Phe Gly Ile Asp	
260	265	270
Leu Tyr Thr Ser Val Phe His Gln Ser	Pro Val Val Phe Gly Ala	
275	280	285
Phe Pro Ser Leu His Ala Ala Asp Ser	Thr Leu Ala Ala Leu Phe	
290	295	300
Met Ser His Val Phe Pro Arg Met Lys	Pro Val Phe Val Thr Tyr	
305	310	315
Thr Leu Trp Met Trp Trp Ala Thr Met	Tyr Leu Ser His His Tyr	
320	325	330
Ala Val Asp Leu Val Ala Gly Gly Leu	Leu Ala Ala Ile Ala Phe	
335	340	345
Tyr Phe Ala Lys Thr Arg Phe Leu Pro	Arg Val Gln Leu Asp Lys	
350	355	360
Thr Phe Arg Trp Asp Tyr Asp Tyr Val	Glu Phe Gly Glu Ser Ala	
365	370	375
Leu Glu Tyr Gly Tyr Gly Ala Ala Gly	Tyr Asp Gly Asp Phe Asn	
380	385	390
Leu Asp Ser Asp Glu Trp Thr Val Gly	Ser Ser Ser Ser Val Ser	
395	400	405
Ser Gly Ser Leu Ser Pro Val Asp Asp	His Tyr Ser Trp Glu Thr	
410	415	420
Glu Ala Leu Thr Ser Pro His Thr Asp	Ile Glu Ser Gly Arg His	
425	430	435
Thr Phe Ser Pro		

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2856 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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cggctcaaag acatcctcgt ttggccgctg gagaccggag cgtgcgcttc gtttcgtctt 180
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taacggcttg ttattcaaga ccccttttct gccgcttcg cgaccgattt attcgtcgcc 300
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gcatatagcg atctcgctcc tcctccactg catctattta cgagacggcg ttagaacatt 1800
tcacgacatt ctggccttat tgcacgagc acatttcgac acatatactt ttaataccct 1860
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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asn Gln Thr Leu Pro Thr Trp Lys Asp Arg Thr Gln Asn Gln

1	5	10	15
Phe Gly Lys Leu Gln Ile Gln Val Pro Trp Arg Ser Ile Gln Leu			
	20	25	30
Leu Val Pro His Arg Met Arg Arg Lys Leu Arg Ser Lys Leu Arg			
	35	40	45
Ser Arg Ala Ser Pro Thr Ser Ser Ile Ala Ser Leu Gln Thr Ser			
	50	55	60
Leu Ser Pro Ala Asp Thr Leu Arg Ser Leu Gln Ser His Arg Trp			
	65	70	75
Thr Val Tyr Asp Phe Gln Tyr Leu Leu Leu Leu Ile Val Gly Ile			
	80	85	90
Phe Ser Leu Thr Val Ile Glu Ser Pro Gly Pro Leu Gly Lys Thr			
	95	100	105
Ala Ile Phe Ser Met Leu Leu Phe Ser Leu Leu Ile Pro Met Thr			
	110	115	120
Arg Gln Phe Phe Leu Pro Phe Leu Pro Ile Ala Gly Trp Leu Leu			
	125	130	135
Phe Phe Tyr Ala Cys Gln Phe Ile Pro Ser Asp Trp Arg Pro Ala			
	140	145	150
Ile Trp Val Arg Val Leu Pro Ala Leu Glu Asn Ile Leu Tyr Gly			
	155	160	165
Ala Asn Ile Ser Asn Ile Leu Ser Ala His Gln Asn Val Val Leu			
	170	175	180
Asp Val Leu Ala Trp Leu Pro Tyr Gly Ile Cys His Tyr Gly Ala			
	185	190	195
Pro Phe Val Cys Ser Leu Ile Met Phe Ile Phe Gly Pro Pro Gly			
	200	205	210
Thr Val Pro Leu Phe Ala Arg Thr Phe Gly Tyr Ile Ser Met Thr			
	215	220	225
Ala Val Thr Ile Gln Leu Phe Phe Pro Cys Ser Pro Pro Trp Tyr			
	230	235	240
Glu Asn Arg Tyr Gly Leu Ala Pro Ala Asp Tyr Ser Ile Gln Gly			

245	250	255
Asp Pro Ala Gly Leu Ala Arg Ile Asp	Lys Leu Phe Gly Ile Asp	
260	265	270
Leu Tyr Thr Ser Gly Phe His Gln Ser	Pro Val Val Phe Gly Ala	
275	280	285
Phe Pro Ser Leu His Ala Ala Asp Ser	Thr Leu Ala Ala Leu Phe	
290	295	300
Met Ser His Val Phe Pro Arg Met Lys	Pro Val Phe Val Thr Tyr	
305	310	315
Thr Leu Trp Met Trp Trp Ala Thr Met	Tyr Leu Ser His His Tyr	
320	325	330
Ala Val Asp Leu Val Ala Gly Gly Leu	Leu Ala Ala Ile Ala Phe	
335	340	345
Tyr Phe Ala Lys Thr Arg Phe Leu Pro	Arg Val Gln Leu Asp Lys	
350	355	360
Thr Phe Arg Trp Asp Tyr Asp Tyr Val	Glu Phe Gly Glu Ser Ala	
365	370	375
Leu Glu Tyr Gly Tyr Gly Ala Ala Gly	Tyr Asp Gly Asp Phe Asn	
380	385	390
Leu Asp Ser Asp Glu Trp Thr Val Gly	Ser Ser Ser Ser Val Ser	
395	400	405
Ser Gly Ser Leu Ser Pro Val Asp Asp	His Tyr Ser Trp Glu Thr	
410	415	420
Glu Ala Leu Thr Ser Pro His Thr Asp	Ile Glu Ser Gly Arg His	
425	430	435
Thr Phe Ser Pro		

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 436 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Asn	Thr	Thr	Leu	Pro	Ser	Trp	Lys	Asp	Arg	Thr	Gln	Asn	Gln
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Phe	Gly	Lys	Leu	Gln	Ile	Gln	Val	Pro	Trp	Arg	Thr	Ile	Gln	Leu
				20				25					30	
Leu	Val	Pro	His	Arg	Met	Arg	Arg	Lys	Ile	Arg	Ser	Lys	Leu	Arg
				35				40					45	
Ser	Arg	Ile	Ser	Pro	Thr	Ser	Ser	Ile	Ser	Ser	Leu	Gln	Thr	Ser
				50				55					60	
Phe	Ser	Pro	Val	Asp	Thr	Leu	Arg	Ser	Leu	Gln	Ser	His	Arg	Trp
				65				70					75	
Thr	Leu	Tyr	Asp	Phe	Gln	Tyr	Leu	Leu	Leu	Ile	Val	Gly	Ile	
				80				85					90	
Phe	Ser	Leu	Ser	Val	Met	Glu	Ser	Pro	Gly	Pro	Leu	Ala	Lys	Thr
				95				100					105	
Ala	Ala	Phe	Thr	Leu	Leu	Leu	Val	Ser	Leu	Leu	Leu	Pro	Ile	Thr
				110				115					120	
Arg	Gln	Phe	Phe	Leu	Pro	Phe	Leu	Pro	Ile	Ala	Gly	Trp	Leu	Ile
				125				130					135	
Phe	Phe	Tyr	Ala	Cys	Gln	Phe	Ile	Pro	Ser	Asp	Trp	Arg	Pro	Ala
				140				145					150	
Ile	Trp	Val	Arg	Val	Leu	Pro	Ala	Leu	Glu	Asn	Ile	Leu	Tyr	Gly
				155				160					165	
Ala	Asn	Ile	Ser	Asn	Ile	Leu	Ser	Ala	His	Gln	Asn	Val	Val	Leu
				170				175					180	
Asp	Val	Leu	Ala	Trp	Leu	Pro	Tyr	Gly	Ile	Cys	His	Tyr	Gly	Ala
				185				190					195	
Pro	Phe	Val	Cys	Ser	Ala	Ile	Met	Phe	Ile	Phe	Gly	Pro	Pro	Gly
				200				205					210	

Thr Val Pro Leu Phe Ala Arg Thr Phe Gly Tyr Ile Ser Met Ala		
	215	220 225
Ala Val Thr Ile Gln Leu Phe Phe Pro Cys Ser Pro Pro Trp Tyr		
	230	235 240
Glu Asn Leu Tyr Gly Leu Ala Pro Ala Asp Tyr Ser Met Pro Gly		
	245	250 255
Asn Pro Ala Gly Leu Ala Arg Ile Asp Glu Leu Phe Gly Ile Asp		
	260	265 270
Leu Tyr Thr Ser Gly Phe Arg Gln Ser Pro Val Val Phe Gly Ala		
	275	280 285
Phe Pro Ser Leu His Ala Ala Asp Ser Thr Leu Ala Ala Leu Phe		
	290	295 300
Met Ser Gln Val Phe Pro Arg Leu Lys Pro Leu Phe Val Ile Tyr		
	305	310 315
Thr Leu Trp Met Trp Trp Ala Thr Met Tyr Leu Ser His His Tyr		
	320	325 330
Ala Val Asp Leu Val Gly Gly Gly Leu Leu Ala Thr Val Ala Phe		
	335	340 345
Tyr Phe Ala Lys Thr Arg Phe Met Pro Arg Val Gln Asn Asp Lys		
	350	355 360
Met Phe Arg Trp Asp Tyr Asp Tyr Val Glu Tyr Gly Asp Ser Ala		
	365	370 375
Leu Asp Tyr Gly Tyr Gly Pro Ala Ser Phe Glu Gly Glu Phe Asn		
	380	385 390
Leu Asp Ser Asp Glu Trp Thr Val Gly Ser Ser Ser Ser Ile Ser		
	395	400 405
Ser Gly Ser Leu Ser Pro Val Asp Asp His Tyr Ser Trp Glu Gly		
	410	415 420
Glu Thr Leu Ala Ser Pro Ala Thr Asp Ile Glu Ser Gly Arg His		
	425	430 435
Phe		

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ala	Asn	Pro	Phe	Ser	Arg	Trp	Phe	Leu	Ser	Glu	Arg	Pro	Pro
1				5					10					15
Asn	Cys	His	Val	Ala	Asp	Leu	Glu	Thr	Ser	Leu	Asp	Pro	His	Gln
				20					25					30
Thr	Leu	Leu	Lys	Val	Gln	Lys	Tyr	Lys	Pro	Ala	Leu	Ser	Asp	Trp
				35					40					45
Val	His	Tyr	Ile	Phe	Leu	Gly	Ser	Ile	Met	Leu	Phe	Val	Phe	Ile
				50					55					60
Thr	Asn	Pro	Ala	Pro	Trp	Ile	Phe	Lys	Ile	Leu	Phe	Tyr	Cys	Phe
				65					70					75
Leu	Gly	Thr	Leu	Phe	Ile	Ile	Pro	Ala	Thr	Ser	Gln	Phe	Phe	Phe
				80					85					90
Asn	Ala	Leu	Pro	Ile	Leu	Thr	Trp	Val	Ala	Leu	Tyr	Phe	Thr	Ser
				95					100					105
Ser	Tyr	Phe	Pro	Asp	Asp	Arg	Arg	Pro	Pro	Ile	Thr	Val	Lys	Val
				110					115					120
Leu	Pro	Ala	Val	Glu	Thr	Ile	Leu	Tyr	Gly	Asp	Asn	Leu	Ser	Asp
				125					130					135
Ile	Leu	Ala	Thr	Ser	Thr	Asn	Ser	Phe	Leu	Asp	Ile	Leu	Ala	Trp
				140					145					150
Leu	Pro	Tyr	Gly	Leu	Phe	His	Phe	Gly	Ala	Pro	Phe	Val	Val	Ala
				155					160					165
Ala	Ile	Leu	Phe	Val	Phe	Gly	Pro	Pro	Thr	Val	Leu	Gln	Gly	Tyr

170	175	180
Ala Phe Ala Phe Gly Tyr Met Asn Leu	Phe Gly Val Ile Met Gln	
185	190	195
Asn Val Phe Pro Ala Ala Pro Pro Trp	Tyr Lys Ile Leu Tyr Gly	
200	205	210
Leu Gln Ser Ala Asn Tyr Asp Met His	Gly Ser Pro Gly Gly Leu	
215	220	225
Ala Arg Ile Asp Lys Leu Leu Gly Ile	Asn Met Tyr Thr Thr Ala	
230	235	240
Phe Ser Asn Ser Ser Val Ile Phe Gly	Ala Phe Pro Ser Leu His	
245	250	255
Ser Gly Cys Ala Thr Met Glu Ala Leu	Phe Phe Cys Tyr Cys Phe	
260	265	270
Pro Lys Leu Lys Pro Leu Phe Ile Ala	Tyr Val Cys Trp Leu Trp	
275	280	285
Trp Ser Thr Met Tyr Leu Thr His His	Tyr Phe Val Asp Leu Met	
290	295	300
Ala Gly Ser Val Leu Ser Tyr Val Ile	Phe Gln Tyr Thr Lys Tyr	
305	310	315
Thr His Leu Pro Ile Val Asp Thr Ser	Leu Phe Cys Arg Trp Ser	
320	325	330
Tyr Thr Ser Ile Glu Lys Tyr Asp Ile	Ser Lys Ser Asp Pro Leu	
335	340	345
Ala Ala Asp Ser Asn Asp Ile Glu Ser	Val Pro Leu Ser Asn Leu	
350	355	360
Glu Leu Asp Phe Asp Leu Asn Met Thr	Asp Glu Pro Ser Val Ser	
365	370	375
Pro Ser Leu Phe Asp Gly Ser Thr Ser	Val Ser Arg Ser Ser Ala	
380	385	390
Thr Ser Ile Thr Ser Leu Gly Val Lys	Arg Ala	
395	400	

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 422 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Ser	Ala	Leu	Ser	Thr	Leu	Lys	Lys	Arg	Leu	Ala	Ala	Cys	Asn
1				5					10					15
Arg	Ala	Ser	Gln	Tyr	Lys	Leu	Glu	Thr	Ser	Leu	Asn	Pro	Met	Pro
				20					25					30
Thr	Phe	Arg	Leu	Leu	Arg	Asn	Thr	Lys	Trp	Ser	Trp	Thr	His	Leu
				35					40					45
Gln	Tyr	Val	Phe	Leu	Ala	Gly	Asn	Leu	Ile	Phe	Ala	Cys	Ile	Val
				50					55					60
Ile	Glu	Ser	Pro	Gly	Phe	Trp	Gly	Lys	Phe	Gly	Ile	Ala	Cys	Leu
				65					70					75
Leu	Ala	Ile	Ala	Leu	Thr	Val	Pro	Leu	Thr	Arg	Gln	Ile	Phe	Phe
				80					85					90
Pro	Ala	Ile	Val	Ile	Ile	Thr	Trp	Ala	Ile	Leu	Phe	Tyr	Ser	Cys
				95					100					105
Arg	Phe	Ile	Pro	Glu	Arg	Trp	Arg	Pro	Pro	Ile	Trp	Val	Arg	Val
				110					115					120
Leu	Pro	Thr	Leu	Glu	Asn	Ile	Leu	Tyr	Gly	Ser	Asn	Leu	Ser	Ser
				125					130					135
Leu	Leu	Ser	Lys	Thr	Thr	His	Ser	Ile	Leu	Asp	Ile	Leu	Ala	Trp
				140					145					150
Val	Pro	Tyr	Gly	Val	Met	His	Tyr	Ser	Ala	Pro	Phe	Ile	Ile	Ser
				155					160					165

Phe Ile Leu Phe Ile Phe Ala Pro Pro Gly Thr Leu Pro Val Trp		
	170	175 180
Ala Arg Thr Phe Gly Tyr Met Asn Leu Phe Gly Val Leu Ile Gln		
	185	190 195
Met Ala Phe Pro Cys Ser Pro Pro Trp Tyr Glu Asn Met Tyr Gly		
	200	205 210
Leu Glu Pro Ala Thr Tyr Ala Val Arg Gly Ser Pro Gly Gly Leu		
	215	220 225
Ala Arg Ile Asp Ala Leu Phe Gly Thr Ser Ile Tyr Thr Asp Gly		
	230	235 240
Phe Ser Asn Ser Pro Val Val Phe Gly Ala Phe Pro Ser Leu His		
	245	250 255
Ala Gly Trp Ala Met Leu Glu Ala Leu Phe Leu Ser His Val Phe		
	260	265 270
Pro Arg Tyr Arg Phe Cys Phe Tyr Gly Tyr Val Leu Trp Leu Cys		
	275	280 285
Trp Cys Thr Met Tyr Leu Thr His His Tyr Phe Val Asp Leu Val		
	290	295 300
Gly Gly Met Cys Leu Ala Ile Ile Cys Phe Val Phe Ala Gln Lys		
	305	310 315
Leu Arg Leu Pro Gln Leu Gln Thr Gly Lys Ile Leu Arg Trp Glu		
	320	325 330
Tyr Glu Phe Val Ile His Gly His Gly Leu Ser Glu Lys Thr Ser		
	335	340 345
Asn Ser Leu Ala Arg Thr Gly Ser Pro Tyr Leu Leu Gly Arg Asp		
	350	355 360
Ser Phe Thr Gln Asn Pro Asn Ala Val Ala Phe Met Ser Gly Leu		
	365	370 375
Asn Asn Met Glu Leu Ala Asn Thr Asp His Glu Trp Ser Val Gly		
	380	385 390
Ser Ser Ser Pro Glu Pro Leu Pro Ser Pro Ala Ala Asp Leu Ile		
	395	400 405

Asp Arg Pro Ala Ser Thr Thr Ser Ser Ile Phe Asp Ala Ser His
410 415 420
Leu Pro

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Ser Ser Ile Leu Arg Ser Lys Ile Ile Gln Lys Pro Tyr
1 5 10 15
Gln Leu Phe His Tyr Tyr Phe Leu Ser Glu Lys Ala Pro Gly Ser
20 25 30
Thr Val Ser Asp Leu Asn Phe Asp Thr Asn Ile Gln Thr Ser Leu
35 40 45
Arg Lys Leu Lys His His His Trp Thr Val Gly Glu Ile Phe His
50 55 60
Tyr Gly Phe Leu Val Ser Ile Leu Phe Phe Val Phe Val Val Phe
65 70 75
Pro Ala Ser Phe Phe Ile Lys Leu Pro Ile Ile Leu Ala Phe Ala
80 85 90
Thr Cys Phe Leu Ile Pro Leu Thr Ser Gln Phe Phe Leu Pro Ala
95 100 105
Leu Pro Val Phe Thr Trp Leu Ala Leu Tyr Phe Thr Cys Ala Lys
110 115 120
Ile Pro Gln Glu Trp Lys Pro Ala Ile Thr Val Lys Val Leu Pro
125 130 135
Ala Met Glu Thr Ile Leu Tyr Gly Asp Asn Leu Ser Asn Val Leu
17

140	145	150
Ala Thr Ile Thr Thr Gly Val Leu Asp Ile Leu Ala Trp Leu Pro		
155	160	165
Tyr Gly Ile Ile His Phe Ser Phe Pro Phe Val Leu Ala Ala Ile		
170	175	180
Ile Phe Leu Phe Gly Pro Pro Thr Ala Leu Arg Ser Phe Gly Phe		
185	190	195
Ala Phe Gly Tyr Met Asn Leu Leu Gly Val Leu Ile Gln Met Ala		
200	205	210
Phe Pro Ala Ala Pro Pro Trp Tyr Lys Asn Leu His Gly Leu Glu		
215	220	225
Pro Ala Asn Tyr Ser Met His Gly Ser Pro Gly Gly Leu Gly Arg		
230	235	240
Ile Asp Lys Leu Leu Gly Val Asp Met Tyr Thr Thr Gly Phe Ser		
245	250	255
Asn Ser Ser Ile Ile Phe Gly Ala Phe Pro Ser Leu His Ser Gly		
260	265	270
Cys Cys Ile Met Glu Val Leu Phe Leu Cys Trp Leu Phe Pro Arg		
275	280	285
Phe Lys Phe Val Trp Val Thr Tyr Ala Ser Trp Leu Trp Trp Ser		
290	295	300
Thr Met Tyr Leu Thr His His Tyr Phe Val Asp Leu Ile Gly Gly		
305	310	315
Ala Met Leu Ser Leu Thr Val Phe Glu Phe Thr Lys Tyr Lys Tyr		
320	325	330
Leu Pro Lys Asn Lys Glu Gly Leu Phe Cys Arg Trp Ser Tyr Thr		
335	340	345
Glu Ile Glu Lys Ile Asp Ile Gln Glu Ile Asp Pro Leu Ser Tyr		
350	355	360
Asn Tyr Ile Pro Val Asn Ser Asn Asp Asn Glu Ser Arg Leu Tyr		
365	370	375
Thr Arg Val Tyr Gln Glu Ser Gln Val Ser Pro Pro Gln Arg Ala		

	380	385	390
Glu Thr Pro Glu Ala Phe Glu Met Ser Asn Phe Ser Arg Ser Arg			
	395	400	405
Gln Ser Ser Lys Thr Gln Val Pro Leu Ser Asn Leu Thr Asn Asn			
	410	415	420
Asp Gln Val Ser Gly Ile Asn Glu Glu Asp Glu Glu Glu Glu Gly			
	425	430	435
Asp Glu Ile Ser Ser Ser Thr Pro Ser Val Phe Glu Asp Glu Pro			
	440	445	450
Gln Gly Ser Thr Tyr Ala Ala Ser Ser Ala Thr Ser Val Asp Asp			
	455	460	465
Leu Asp Ser Lys Arg Asn			
	470		

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: /note= "Xaa at position 3 is Val or Ile"

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: /note= "Xaa at position 7 is Leu or Val"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Leu Asp Xaa Leu Ala Trp Xaa Pro Tyr Gly

1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Phe Gly Ala Phe Pro Ser Leu His

1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION: /note= "Xaa at position 5 is Ser or Thr"

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION: /note= "Xaa at position 9 is Ala or Phe"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Thr Met Tyr Leu Xaa His His Tyr Xaa Val Asp Leu

1

5

10

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2935 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
atatttcttcc ccataacaac tcttctcgcc cttcctccgg ctccgtggcc aaattgtttt 60
atgcagcgcc tcctagcgat ttaacctcgt tctcgttgcc cttgcctgtc cgccttgcggt 120
cagtagcacc cttgcaacgt gaccttcccc agagtatcct cgtttgggcg ctggagaccg 180
gagcttgcac cctcataaac tagctcttcg aaatcaattc tccgttctcc agagattatc 240
ggatcgaatc tctccgctgt cgacaccttt cgtctctcgg tgatcctcgc ccttgaggatc 300
tcgtcacgtt gacgccttga acccctggcc gccaaactcca cataggagac cacacttcat 360
tcttcccccg ccataattgc agcaccctcc gtctcccttc gagtcctcc tggatcatca 420
agtccgaaag gattagactc gtcgcagcga tgaataccac cttccatcc tgggaaggatc 480
ggacgcaaaa ccagttcggc aagctccaga tccaagtccc atggcgcacc atacaacttc 540
tcgtgccgca ccgtatgcga cggaagattc ggtccaagct gcgcagtcgg atctcgccta 600
cctcatcgat atcctcgttg cagacgtcat tctcacctgt cgatacactc aggtcgctgc 660
aaagtcatag atggacgctc tatgactttc agtatctttt gctgctgatt gtcggcatat 720
tctcgctgag cgttatggaa tcacctggac cattggcaaa gaccgccgcy tttacgctac 780
ttctcgtctc tctccttctc ccgattacgc gccagttctt cttgccattc ctcccgattg 840
caggatggct tatatttttc tacgcttgcc agttcatccc gagcgactgg cgccctgcaa 900
tctgggttcg cgtgctgccc gctctggaaa acattctcta cggtgctaata atcagtaaca 960
tcctttccgc tcacaaaaat gtggtgcttg acgttttggc gtggcttccc tacggaatct 1020
```

gccattatgg cgcgccatth gtgtgctcag cgatcatgtt catcttttgg cctcccggca 1080
ccgtccccct tttcgctcga acttttggat acatcagcat ggctgcagtc accattcagc 1140
tgtttttccc ctgctctcct ccgtggtacg aaaatctgta tggtttggct ccggctgatt 1200
actccatgcc gggtaatcct gcgggccttg ctcgcatcga tgagcttttt gggatagact 1260
tgtacacatc gggcttcaga caatctcccg tcgtgtttgg cgcatttcct tccctacatg 1320
ccgtgattc gacacttgca gctctattta tgagccaagt gttcccacgg ttgaagccct 1380
tgtttgtcat ctatactctc tggatgtggg gggctacaat gtatctttcg caccactacg 1440
ctgttgatct ggtcgggtgg ggcctcttgg caactgtcgc gttctacttt gctaaaacgc 1500
ggttcatgcc tcgcgtccag aatgataaga tgttccgctg ggactacgat tatgttgagt 1560
acggcgattc cgcactcgac tatgggtacg gtccagccag cttcgaaggc gaattcaacc 1620
ttgatagcga tgagtggacc gttggttctt cgtcatccat ttcgtccggc tccctcagtc 1680
cagttgacga ccactactct tgggagggcg agactcttgc ctctcctgcc accgacatcg 1740
agtctggaag gcatttctga tcctgctcaa tgagccttga tacgtactac actgtgtacg 1800
tgctactgca ttgactaatg agacggcggt ttcaaacaaa ttttaacgac atgcttggtt 1860
atcgcattga gctgatttcg acacatatat atgtttaata cgttttgggg aactccagg 1920
gattcatgac ggttgcttca tatcccgacc tggggatgga ttgacctggg tgtgcccaat 1980
tttcttctgc ctaacgtttt gattatacat gcatttttca cgaaaccagc cggcccgcga 2040
tgatcgtgac ctcaatttga gctcgaatct tcctggggcc tccagcgata attcttaatg 2100
ctcgttccga ggggtgccaca tcggacattc gcttgtagaa cttttgcaga acgaacattt 2160
tcaccgattc caacttgagt cattcgctta ctactttcaa ctggtcgaga aacttcgctt 2220
cttttcagct cggctaggtg cataaatatt ttacattcgt gtcgatcgct cacatttcac 2280
ggcgcctgga aacttggggg tttcgatttc attggaagg ataaacaaca tgggctgggc 2340
gccttttaca cgcactacat tcgcttagaa aagttctgat gcttttaatg attcttgcac 2400
tggcatatag aaaggggtcc tccagactcg ctactgtggg cctctctcaa cccacactc 2460
gcttgctttt aacagtggac accccgtgga gctacgtctc catcaaata ttggcatcaa 2520
ccggaatcga tgccaggagg actgagctta ctcacggtga ccgtcgggta aaaggcgctt 2580
atacagaaca tctcctctat cctcctgtcc catctcgatt ctctggctgc tggacgcaac 2640
acacctcgct gcacgttttc gacttcctaa tacgacctaa tatcattctc ggttttcttt 2700
gctctggctc gcggccgcca tttatatggc gtgtcggctc gagtctgaag tgaacttttt 2760
tctcctttct ggcctccaca actttccgat ccctagcagc ttcccgtgca cagcgaggtg 2820
ttgttggatg attgttccat agcattatca ttattcctaa tccggtagcg ttatgattta 2880
tgaagaacag tgatgtacat tattatgcgg tgatcaaaaa aaaaaaaaaa aaaaa 2935

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2856 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iv) ANTI-SENSE: Yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
tagtatacaa gttgccttca taaatcataa cactaccgga ttataactaa taatactgct 60
gctatggata atttgcccca accacacaca cacacacact atccaaggga aacgaaaaga 120
agaggatagt gtccatgagc ggaatttgtg aggtgaggag gatgtgatag gtaggtgtga 180
gagcgtcaga ccatagcaag caagtcaagt caccgtccaa caagtcgaga atctgaggtt 240
agtcgaagcc ggggtcaaac gggacgcgtg aacatccttc aacaagcccc gtcagcgtca 300
gactctcttc ccaaccttgc acgtccggcg aatgtcagaa agcaacacag tagccatgtg 360
tatagcccc gggtaatatg tggacgtaat ccactttgag cgaatggata aaccatgcga 420
gcaatcaaga agaaggtcca tccttccctt ctttctatat gctaattgag agttcgtgat 480
gcattgcaaa gcagaaatgt aaaaccgtct atgcacagcg agtgaagtgc aagaagaaaa 540
ggcgccccat tccgtgattt tttccaatat aaatgcttcc agtcccaagc gccaagagta 600
tgagcgatcg acacgaatgg taaaaataaa tatatagcat agtcgaaacg aataataagg 660
atgggttcga ccaggtcaag gtaatagcgg acgatagaag tgagaattga agtagtgtct 720
gggtggacac gagacaagcg agtgttaccg acgggggtta tcggatggtc ttccaggact 780
aaacaccagg atgcgtagcc ccattgtgtc cattaacatt atgatggagc aacggcgtgt 840
agcgatgagc gataacccat cccacgttcg agcccaaccc ggtttcgcaa tgtcaagcaa 900
tgtacagtga agtgcgggcg aaagagaaac agtatcccag gcggattcgg accgaggtac 960
attaaggctc aaccgatgat ctgggacacc gaagaaaggg tattaagat atatgtgtcg 1020
aaatgtgctc gatgcaataa agccagaatg tcgtgaaatg ttctaacgcc gtctcgtaaa 1080
tagatgcagt ggaggaggag cgagatcgct atatgcaggt atcgagtttg gtttgtggct 1140
actcaagggc tgaaagtatg cctgccggac tcaatatcag tatgtgggga ggtcagtgcc 1200
tcggtttccc atgagtaatg atcgtcaacg ggactcaagg agcctgagga gacggaggat 1260
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gaagaaccaa cagtccattc atcgctgtcg agattgaagt ctccatcata gccagctgca 1320
ccatacccat actccagggc agactcgccg aattccacat agtcgtagtc ccaacggaag 1380
gtcttgtcga gctggacacg gggaaggaat cgggtcttgg cgaagtagaa agcaatggcg 1440
gccaggagac caccgcgaac caaatcgacc gcatagtgat gtgagaggta cattgttgcc 1500
caccacatcc atagagtata ggtcacgaag acgggcttca tgcgggggaa aacatgactc 1560
atgaaaagtg cggccagggg tgagtcggca gcatgcagcg acgaaaaagc gccgaacaca 1620
acaggcgact gatggaaaac agacgtgtaa aggtcgatgc cgaaaagctt gtcaatgcgg 1680
gcaagccctg cgggatcacc ttggatggag tagtctgccg gagctagacc atagcgattc 1740
tcataccaag gtggagagca agggaaaaac agctgaatag taaccgcagt catactgata 1800
tagccgaaag tgcgcgcgaa aaggggaaca gtgccgggcg gaccgaagat gaacatgata 1860
aacgagcaca caaacggagc gccatagtgg cagataccgt agggtagcca cgccagcacg 1920
tcaagcaca cgttctggtg agcggatagg atgttgctga tgtttgccg gtagagaata 1980
ttctccagt caggcaagac acgaaccaa atcgagggc gccaatcgct tgggatgaac 2040
tggcaggcgt agaaaaacag aagccatccg gcaatcggca gaaacgggag gaagaactgg 2100
cgggtcatag ggatcaggag agagaatagg agcatggaga aaatggccgt tttgccccaa 2160
ggcccgggcg actcgataac ggtcaaagag aagatgccca cgatcaacag aagcagatat 2220
tggaagtcgt aaaccgtcca tcggtggctt tggagcgatc gtagtgtgtc tgcaggcgat 2280
aacgacgtct gtaaagaggc tattgacgag gtaggagacg ctctactgcg caatttggac 2340
cttaacttcc gccgcatgcg atcggggacg agcagttgga tggaccgcca tggaacctgg 2400
atctgaagct ttccaaactg gttctgctg cggtccttcc acgtgggaag tgtttgattc 2460
atggttgccg cgagtcttgc gggcaagact cagctataat tcctccagat cgaactccgt 2520
ctgctttctt tcccccgat tgtacaagag ttggaaggcg acgaataaat cggtcgaggc 2580
agcggcagaa aaggggtctt gaataacaag ccgttaggca acgagcaggg tgctgacggc 2640
gtcaaccgga gcgggggaaat tgagatcggg tcgaagaaga cgaaacgaag cgcacgctcc 2700
ggtctccagc ggccaaacga ggatgtctt gagccgtcac gttgcagggg gtttactga 2760
tgcaaggcga agtgcaaggc cgcagcagtc gagaggaaaa cctggaacga ggaggtcgtg 2820
agggaggcag atggccacgg agccggagta taaacc 2856

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(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2856 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: mRNA

(iv) ANTI-SENSE: Yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
uaguauacaa guugccuuca uaaaucauaa cacuaccgga uuauaacuaa uaauacugcu 60
gcuauaggaua auuugcccca accacacaca cacacacacu auccaaggga aacgaaaaga 120
agaggauagu guccaugagc ggaauuugug aggugaggag gaugugauag guagguguga 180
gagcgucaga ccuagcaag caagucaagu caccguccaa caagucgaga aucugagguu 240
agucgaagcc gggucaaauc gggacgcgug aacauccuuc aacaagcccc gucagcguca 300
gacucuccuc ccaaccuugc acguccggcg aaugucagaa agcaacacag uagccaugug 360
uauagcccc ggguaauaug uggacguaau ccacuuugag cgaauaggaua aaccaugcga 420
gcaaucaaga agaaggucca uccuuccccu cuuucuaauu gcuaaugcag aguucgugau 480
gcauugcaaa gcagaaaugu aaaaccgucu augcacagcg agugaagugc aagaagaaaa 540
ggcgccccau uccgugauuu uuuccaauau aaugcuucc agucccaagc gccaaagagua 600
ugagcgaucg acacgaauug uaaaaauaaa uauauagcau agucgaaacg aauaauaagg 660
auggguuca ccaggucaag guaauagcgg acgauagaag ugagaauuga aguagugucu 720
ggguggacac gagacaagcg aguguuaccg acggggguua ucggaugguc uuccaggacu 780
aaacaccagg augcguagcc ccauuguguc cauuacauu augauggagc aacggcgugu 840
agcgaugagc gauaaccuau cccacguucg agcccaaccc gguuucgcaa ugucaagcaa 900
uguacaguga agugcgggcg aaagagaaac aguaucccag gcggauucgg accgagguac 960
auuaaggucg aaccgaugau cugggacacc gaagaaaggg uauuaaagau auaugugucg 1020
aaugugcuc gaugcaauaa agccagaauug ucgugaaaug uucuaacgcc gucucguaaa 1080
uagaugcagu ggaggaggag cgagaucgcu auaugcaggu aucgaguug guuuguggcu 1140
acucaagggc ugaaaguaug ccugccggac ucaauaucag uaugugggga ggucagugcc 1200
ucgguuuccc augaguaauug aucgucaacg ggacucaagg agccugagga gacggaggau 1260
gaagaaccaa caguccauuc aucgcugucg agauugaagu cuccaucua gccagcugca 1320
ccauaccuau acuccagggc agacucgccg aaauccacau agucguaguc ccaacggaag 1380
gucuugucga gcuggacacg gggaaaggau cgggucuugg cgaaguagaa agcaauggcg 1440
gccaggagac cccccgaac caaauccgacc gcauagugau gugagaggua cauuguugcc 1500
caccacaucc auagaguaua ggucacgaag acgggcuuca ugcgggggaa acaugacuc 1560
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augaaaagug cggccagggg uagagucggca gcaugcagcg acggaaaagc gccgaacaca 1620
acaggcgacu gauggaaaac agacguguaa aggucgaugc cgaaaagcuu gucaaugcgg 1680
gcaagcccug cgggaucacc uuggauggag uagucugccg gagcuagacc auagcgauuc 1740
ucauaccaag guggagagca agggaaaaac agcugaauag uaaccgcagu cauacugaua 1800
uagccgaaag ugcgcgcgaa aaggggaaca gugccgggcg gaccgaagau gaacaugauc 1860
aacgagcaca caaacggagc gccauagugg cagauaccgu aggguaagcca cgccagcacg 1920
ucaagcacia cguucuggug agcggauagg auguugcuga uguuugcgcc guagagaaua 1980
uucuccagug caggcaagac acgaacccaa aucgcagggc gccaaucgcu ugggaugaac 2040
uggcaggcgu agaaaaacag aagccauccg gcaaucggca gaaacgggag gaagaacugg 2100
cgggucauag ggaucaggag agagaauagg agcauggaga aaauggccgu uuugcccaa 2160
ggcccgggcg acucgauaac ggucaaagag aagaugccca cgaucaacag aagcagauau 2220
uggaagucgu aaaccgucca ucgguggcuu uggagcgau cguaguguguc ugcaggcgau 2280
aacgacgucu guaaagaggc uauugacgag guaggagacg cucuacugcg cauuuuggac 2340
cuuaacuucc gccgcaugcg augcgggacg agcaguugga uggaccgcca uggaaccugg 2400
aucugaagcu uuccaaacug guucugcgug cgguccuucc acgugggaag uguuugauuc 2460
augguugcgg cgagucuugc gggcaagacu cagcuauaa uccuccagau cgaacuccgu 2520
cugcuuuuuu ucccccgau uguacaagag uuggaaggcg acgaauaaau cggucgcgga 2580
agcggcgaaa aaggggucuu gaauaacaag ccguuaggca acgagcaggg ugcugacggc 2640
gucaacccga gcgggggaaau ugagaucggu ucgaagaaga cgaaacgaag cgcacgcucc 2700
ggucuccagc ggccaaacga ggaugucuuu gagccgucac guugcagggg guuucacuga 2760
ugcaaggcga agugcaaggg cgcagcaguc gagaggaaaa ccuggaacga ggaggucgug 2820
agggaggcag auggccacgg agccggagua uaaacc 2856

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(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

aagctttttt	gcctctgcaa	aagttccttt	ctcgaattgg	ttttttgagg	aaaagcaagt	60
taataaacta	attatattat	atataattag	caattttata	aaaaaaataa	aaaaatagcc	120
ctgattgctg	gcaactgtga	gctgaacatt	ggttaatcgg	tccatctttt	tttaaataatt	180
ttacatcgct	acttttaagt	gcttgacact	tgcatttaat	agctactttc	tttccttcat	240
aaaaattcct	tttttttcct	ttagttttcc	ggttaattcc	ttacgaaatt	tttttcgtac	300
gcttcccttt	tttactctga	taattctttg	aagcaatgtc	tgctctttcg	accttaaaaa	360
agcgccttgc	tgcggtgaac	cgagcatccc	aatacaagtt	ggaaacaagc	ttaaacccta	420
tgccctacatt	tcgtttgcta	cgcaatacga	aatgggtcatg	gacacatttg	caatatgtgt	480
ttctagcagg	taatttgatt	tttgcttgta	ttgtcattga	atctcctgga	ttctggggga	540
aatttggcat	tgccctgtctt	ttggccattg	cgttgaccgt	tcctttaaca	cgccaaattt	600
tttttcctgc	cattgttatc	atcacctggg	caattttatt	ttactcttgt	aggtttattc	660
cagaacgctg	gcgtccaccc	atatgggttc	gtgttttacc	cacacttgaa	aatattcttt	720
atggctctaa	tctttctagt	cttctctcga	aaaccacgca	tagcatcctt	gatattttgg	780
cctgggttcc	atatggagtc	atgcattatt	cggctccttt	tatcatttca	tttattcttt	840
tcattctttgc	acctcctgga	actcttccag	tttgggctcg	aacttttggg	tatatgaatt	900
tatttgggtg	tcttatccaa	atggctttcc	cctgttctcc	tccttggtat	gaaaatatgt	960
atggtttaga	acctgccacg	tatgcagtac	gtggctctcc	tggtggattg	gcccgtattg	1020
atgctctctt	cggcactagc	atttacactg	attgtttttc	taactctccg	gttgtttttg	1080
gtgcctttcc	atctcttcac	gctggatggg	ccatgctgga	agcacttttc	ctttcgcatg	1140
tgtttcctcg	ataccgcttc	tgcttttatg	gatatgttct	atggctttgc	tggtgtacta	1200
tgtaccttac	ccaccactac	tttgtagatt	tggtcggcgg	tatgtgttta	gctattatat	1260
gcttcgtttt	tgctcaaaaag	ctacgcctcc	cacagttgca	aactggtaaa	atccttcggt	1320
gggaatacga	gtttgttatc	cacgggtcatg	gtctttccga	aaaaaccagc	aactccttgg	1380
ctcgtaccgg	cagcccatac	ttacttggaa	gggattcttt	tactcaaaac	cctaatgcag	1440
tagccttcat	gagtgggtctt	aacaatatgg	aacttgctaa	caccgatcat	gaatgggtccg	1500
tggtttcatc	atcacctgag	ccgttaccta	gtcctgctgc	tgatttgatt	gatcgtcctg	1560
ccagtaccac	ttcctccatc	tttgatgcaa	gtcatcttcc	ttaaatcaac	gtgctttaag	1620
aatatatttc	caaaagctac	atgatacatt	gactagaatc	ggtttgattc	atagtgggat	1680
tggaatgatg	ttgttcattg	tgttttttaa	ctgttaatct	gacatccatt	gagtcattct	1740
ttacaatttg	taaaattaat	ttgtatcact	aattttgaag	gaagctattt	tggtattaat	1800
accgcttttg	gtctccactt	ccttttcgaa	actcttaaca	gcgattaggc	cgggtatctt	1860
ccagtgtgat	gtataggtat	ttgtcgtttt	tttatcattt	ccgttaataa	agaactcttt	1920

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tatccagctt cttacactgt caactgttgt gaaaggaaca catttagaat ttcattttcc 1980
ttattttgttg tgatttaaatt cgtttgacat aattttaaat ttggtttgaa atgtgtgtga 2040
gaaggcttgt tttattcatt tagttttattg cttgtttgca cgaaaatcca gaacggagca 2100
ttaatgtaat ccttttttat tctgtaaagc gtttttatac aaatgttggt tatacgtttc 2160
taaaataaga atattgttat aataatatag ttttttctat catttggtac acacactaaa 2220
gagacattaa ggataagcaa atgtgttaaa atgataatat attttggaaa catttataaa 2280
gaaattaagc agctttgact aactacattt ttgttttttt cctaagcaaa actgtatagt 2340
tatacacgcg agctgtattc acttccattg tagtgacttg agctc 2385

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(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 422 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Met Ser Ala Leu Ser Thr Leu Lys Lys Arg Leu Ala Ala Cys Asn
  1             5             10             15
Arg Ala Ser Gln Tyr Lys Leu Glu Thr Ser Leu Asn Pro Met Pro
             20             25             30
Thr Phe Arg Leu Leu Arg Asn Thr Lys Trp Ser Trp Thr His Leu
             35             40             45
Gln Tyr Val Phe Leu Ala Gly Asn Leu Ile Phe Ala Cys Ile Val
             50             55             60
Ile Glu Ser Pro Gly Phe Trp Gly Lys Phe Gly Ile Ala Cys Leu
             65             70             75
Leu Ala Ile Ala Leu Thr Val Pro Leu Thr Arg Gln Ile Phe Phe
             80             85             90
Pro Ala Ile Val Ile Ile Thr Trp Ala Ile Leu Phe Tyr Ser Cys
             95             100            105

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Arg Phe Ile Pro Glu Arg Trp Arg Pro Pro Ile Trp Val Arg Val		
	110	115 120
Leu Pro Thr Leu Glu Asn Ile Leu Tyr Gly Ser Asn Leu Ser Ser		
	125	130 135
Leu Leu Ser Lys Thr Thr His Ser Ile Leu Asp Ile Leu Ala Trp		
	140	145 150
Val Pro Tyr Gly Val Met His Tyr Ser Ala Pro Phe Ile Ile Ser		
	155	160 165
Phe Ile Leu Phe Ile Phe Ala Pro Pro Gly Thr Leu Pro Val Trp		
	170	175 180
Ala Arg Thr Phe Gly Tyr Met Asn Leu Phe Gly Val Leu Ile Gln		
	185	190 195
Met Ala Phe Pro Cys Ser Pro Pro Trp Tyr Glu Asn Met Tyr Gly		
	200	205 210
Leu Glu Pro Ala Thr Tyr Ala Val Arg Gly Ser Pro Gly Gly Leu		
	215	220 225
Ala Arg Ile Asp Ala Leu Phe Gly Thr Ser Ile Tyr Thr Asp Cys		
	230	235 240
Phe Ser Asn Ser Pro Val Val Phe Gly Ala Phe Pro Ser Leu His		
	245	250 255
Ala Gly Trp Ala Met Leu Glu Ala Leu Phe Leu Ser His Val Phe		
	260	265 270
Pro Arg Tyr Arg Phe Cys Phe Tyr Gly Tyr Val Leu Trp Leu Cys		
	275	280 285
Trp Cys Thr Met Tyr Leu Thr His His Tyr Phe Val Asp Leu Val		
	290	295 300
Gly Gly Met Cys Leu Ala Ile Ile Cys Phe Val Phe Ala Gln Lys		
	305	310 315
Leu Arg Leu Pro Gln Leu Gln Thr Gly Lys Ile Leu Arg Trp Glu		
	320	325 330
Tyr Glu Phe Val Ile His Gly His Gly Leu Ser Glu Lys Thr Ser		
	335	340 345

Asn Ser Leu Ala Arg Thr Gly Ser Pro Tyr Leu Leu Gly Arg Asp		
	350	355 360
Ser Phe Thr Gln Asn Pro Asn Ala Val Ala Phe Met Ser Gly Leu		
	365	370 375
Asn Asn Met Glu Leu Ala Asn Thr Asp His Glu Trp Ser Val Gly		
	380	385 390
Ser Ser Ser Pro Glu Pro Leu Pro Ser Pro Ala Ala Asp Leu Ile		
	395	400 405
Asp Arg Pro Ala Ser Thr Thr Ser Ser Ile Phe Asp Ala Ser His		
	410	415 420
Leu Pro		

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

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aagctttttt gcctctgcaa aagttccttt ctcgaattgg ttttttgagg aaaagcaagt 60
taataaacta attatattat atataattag caattttata aaaaaaataa aaaaatagcc 120
ctgattgctg gcaactgtga gctgaacatt ggттаатсgg tccatctttt tttaaатatt 180
ttacatcgct acttttaagt gcttgacact tgcatttaat agctactttc tttccttcat 240
aaaaattcct tttttttcct ttagttttcc ggттаатtcc ttacgaaatt tttttcgtag 300
gcttcccttt tttactctga таатtctttg aagcaatgtc tgctctttcg accttaaaaa 360
agcgccttgc tgcgtgtaac cgagcatccc aatacaagtt ggaaacaagc ttaaacccta 420
tgcctacatt tcgtttgcta cgcaatacga aatgggtcatg gacacatttg caatatgtgt 480
ttctagcagg таатttgatt tttgcttgta ttgtcattga atctcctgga ttctggggga 540
aatttggcat tgcctgtctt ttggccattg cgttgaccgt tcctttaaca cgccaaattt 600
ttttcctgc cattgttatc atcacctggg caattttatt ttactcttgt aggtttattc 660

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cagaacgctg gcgtccaccc atatgggttc gtgttttacc cacacttgaa aatattcttt 720
atggctctaa tctttctagt cttctctcga aaaccacgca tagcatcctt gatattttgg 780
cctgggttcc atatggagtc atgcattatt cggctccttt tatcatttca tttattcttt 840
tcatctttgc acctcctgga actcttccag tttgggctcg aacttttggt tatatgaatt 900
tatttggtgt tcttatccaa atggctttcc cctgttctcc tccttggtat gaaaatatgt 960
atggtttaga acctgccacg tatgcagtac gtggctctcc tgggtggattg gcccgtattg 1020
atgctctctt cggcactagc atttacctg atggtttttc taactctccg gttgtttttg 1080
gtgcctttcc atctcttcac gctggatggg ccatgctgga agcacttttc ctttcgcatg 1140
tgtttcctcg ataccgcttc tgcttttatg gatatgttct atggctttgc tgggtgtacta 1200
tgtaccttac ccaccactac tttgtagatt tggtcggcgg tatgtgttta gctattatat 1260
gcttcgtttt tgctcaaaag ctacgcctcc cacagttgca aactggtaaa atccttcggt 1320
gggaatacga gtttgttatc cacggtcattg gtctttccga aaaaaccagc aactccttgg 1380
ctcgtaccgg cagcccatac ttacttgaa gggattcttt tactcaaaac cctaatgcag 1440
tagccttcat gagtggctct aacaatatgg aacttgctaa caccgatcat gaatggtccg 1500
tggtttcatc atcacctgag ccgttaccta gtcctgctgc tgatttgatt gatcgtcctg 1560
ccagtaccac ttctccatc tttgatgcaa gtcacttcc ttaaatacaac gtgctttaag 1620
aatatatttc caaaagctac atgatacatt gactagaatc ggtttgattc atagtgggtat 1680
tggaatgatg ttgttcattg tgttttttaa ctgttaatct gacatccatt gagtcattct 1740
ttacaatttg taaaattaat ttgtatcact aattttgaag gaagctattt tgggtattaat 1800
accgcttttg gtctccactt ctttttcgaa actcttaaca gcgattaggc cgggtatctt 1860
ccagtgtgat gtataggtat ttgtcgtttt tttatcattt ccgttaataa agaactcttt 1920
tatccagctt cttaactgt caactgttgt gaaaggaaca catttagaat ttcattttcc 1980
ttatttggtg tgatttaaatt cgtttgacat aattttaaat ttggtttgaa atgtgtgtga 2040
gaaggcttgt tttattcatt tagtttattg cttgtttgca cgaaaatcca gaacggagca 2100
ttaatgtaat ctttttttat tctgtaaagc gtttttatac aaatgttgggt tatacgtttc 2160
taaaataaga atattgttat aataatatag ttttttctat catttggtac acacactaaa 2220
gagacattaa ggataagcaa atgtgttaaa atgataatat attttggaag catttataaa 2280
gaaattaagc agctttgact aactacattt ttgttttttt cctaagcaaa actgtatagt 2340
tatacacgcg agctgtattc acttccattg tagtgacttg agctc 2385

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(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met	Ser	Ala	Leu	Ser	Thr	Leu	Lys	Lys	Arg	Leu	Ala	Ala	Cys	Asn
1			5						10					15
Arg	Ala	Ser	Gln	Tyr	Lys	Leu	Glu	Thr	Ser	Leu	Asn	Pro	Met	Pro
			20						25					30
Thr	Phe	Arg	Leu	Leu	Arg	Asn	Thr	Lys	Trp	Ser	Trp	Thr	His	Leu
			35						40					45
Gln	Tyr	Val	Phe	Leu	Ala	Gly	Asn	Leu	Ile	Phe	Ala	Cys	Ile	Val
			50						55					60
Ile	Glu	Ser	Pro	Gly	Phe	Trp	Gly	Lys	Phe	Gly	Ile	Ala	Cys	Leu
			65						70					75
Leu	Ala	Ile	Ala	Leu	Thr	Val	Pro	Leu	Thr	Arg	Gln	Ile	Phe	Phe
			80						85					90
Pro	Ala	Ile	Val	Ile	Ile	Thr	Trp	Ala	Ile	Leu	Phe	Tyr	Ser	Cys
			95						100					105
Arg	Phe	Ile	Pro	Glu	Arg	Trp	Arg	Pro	Pro	Ile	Trp	Val	Arg	Val
			110						115					120
Leu	Pro	Thr	Leu	Glu	Asn	Ile	Leu	Tyr	Gly	Ser	Asn	Leu	Ser	Ser
			125						130					135
Leu	Leu	Ser	Lys	Thr	Thr	His	Ser	Ile	Leu	Asp	Ile	Leu	Ala	Trp
			140						145					150
Val	Pro	Tyr	Gly	Val	Met	His	Tyr	Ser	Ala	Pro	Phe	Ile	Ile	Ser
			155						160					165
Phe	Ile	Leu	Phe	Ile	Phe	Ala	Pro	Pro	Gly	Thr	Leu	Pro	Val	Trp
			170						175					180
Ala	Arg	Thr	Phe	Gly	Tyr	Met	Asn	Leu	Phe	Gly	Val	Leu	Ile	Gln

	185	190	195
Met Ala Phe Pro Cys Ser Pro Pro Trp Tyr Glu Asn Met Tyr Gly			
	200	205	210
Leu Glu Pro Ala Thr Tyr Ala Val Arg Gly Ser Pro Gly Gly Leu			
	215	220	225
Ala Arg Ile Asp Ala Leu Phe Gly Thr Ser Ile Tyr Thr Asp Gly			
	230	235	240
Phe Ser Asn Ser Pro Val Val Phe Gly Ala Phe Pro Ser Leu His			
	245	250	255
Ala Gly Trp Ala Met Leu Glu Ala Leu Phe Leu Ser His Val Phe			
	260	265	270
Pro Arg Tyr Arg Phe Cys Phe Tyr Gly Tyr Val Leu Trp Leu Cys			
	275	280	285
Trp Cys Thr Met Tyr Leu Thr His His Tyr Phe Val Asp Leu Val			
	290	295	300
Gly Gly Met Cys Leu Ala Ile Ile Cys Phe Val Phe Ala Gln Lys			
	305	310	315
Leu Arg Leu Pro Gln Leu Gln Thr Gly Lys Ile Leu Arg Trp Glu			
	320	325	330
Tyr Glu Phe Val Ile His Gly His Gly Leu Ser Glu Lys Thr Ser			
	335	340	345
Asn Ser Leu Ala Arg Thr Gly Ser Pro Tyr Leu Leu Gly Arg Asp			
	350	355	360
Ser Phe Thr Gln Asn Pro Asn Ala Val Ala Phe Met Ser Gly Leu			
	365	370	375
Asn Asn Met Glu Leu Ala Asn Thr Asp His Glu Trp Ser Val Gly			
	380	385	390
Ser Ser Ser Pro Glu Pro Leu Pro Ser Pro Ala Ala Asp Leu Ile			
	395	400	405
Asp Arg Pro Ala Ser Thr Thr Ser Ser Ile Phe Asp Ala Ser His			
	410	415	420

Leu Pro

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2340 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
tttctttctg tcaaagaata ataaagtgcc catcagtgtt catatttggt acaaagtgg 60
tttctgattt ggtactactg cagaggcgta ttttttgctt cagttacat agcgtaagaa 120
cactagcgac ttttgttcgt gaaccaacag agtaggattt ctactgctac atctcttagg 180
tagttggtta gtccgatcgc tcacttttgg ttgttgtaa gtacttcata agtttatacct 240
tttccttttt cacttgagc tactttgggt atagcttttg gcccaaggat ctttgaattt 300
tctccaaaag tactttattt tatatcctac aggttgcggt tttcatattt taaaaagctt 360
tttaatcatt cttttgcgta tggcaaacc tttttcgaga tggtttctat cagagagacc 420
tccaaactgc catgtagccg atttagaaac aagtttagat ccccatcaaa cgttggtgaa 480
ggtgcaaaaa tacaaaccg ctttaagcga ctgggtgcat tacatcttct tgggatccat 540
catgctgttt gtgttcatta ctaatccgc acctggatc ttcaagatcc ttttttattg 600
tttcttgggc actttattca tcattccagc tacgtcacag tttttcttca atgccttgcc 660
catcctaaca tgggtggcgc tgtatttcac ttcacgtac tttccagatg accgcaggcc 720
tcctattact gtcaaagtgt taccagcggg ggaacaatt ttatacggcg acaatttaag 780
tgatattctt gcaacatcga cgaattcctt tttggacatt ttagcatggg taccgtacgg 840
actatttcat tatggggccc catttgctgt tgctgccatc ttattcgtat ttgggtccacc 900
aactgttttg caagggtatg cttttgcatt tgggtatatg aacctgtttg gtgttatcat 960
gcaaaatgtc tttccagccg ctcccccatg gtataaaatt ctctatggat tgcaatcagc 1020
caactatgat atgcatgggt cgcctgggtg attagctaga attgataagc tactcgggtat 1080
taatatgat actacagctt tttcaaattc ctccgtcatt ttcggtgctt ttccttcact 1140
gcattccggg tgtgctacta tggaagccct gtttttctgt tattgttttc caaaattgaa 1200
gcccttgttt attgcttatg tttgctggtt atgggtggta actatgtatc tgacacacca 1260
ttattttgta gaccttatgg caggttctgt gctgtcatatc gttattttcc agtacacaaa 1320
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gtacacacat ttaccaattg tagatacatc tcttttttgc agatgggtcat acacttcaat 1380
 tgagaaatac gatatatcaa agagtgatcc attggctgca gattcaaacg atatcgaaag 1440
 tgtccctttg tccaacttgg aacttgactt tgatcttaat atgactgatg aaccagtggt 1500
 aagcccttcg ttatttgatg gatctacttc tgtttctcgt tcgtccgcca cgtctataac 1560
 gtcactaggt gtaaagaggg cttaatgagt attttatctg caattacgga tacggttggt 1620
 cttatgtaga tacatataaa tatatatctt tttctttctt tttcttagtc aggattgtcg 1680
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 ataaattttt gaaataaatg ggtggctttt aatgggtgtct atgttaagtg aggcttttag 1800
 aatgctcttc ctgctttggt tattatatgt gtatgaaaga tatgtatgta ttacatgtg 1860
 tttgtagcgt cccagtcga aacctgtgcg ctatacctaa atggattgat aatcttcatt 1920
 cactaattct aaaatagact tcttcccaa agaacgggtg aacgatgagg ctctatccag 1980
 ctgcttatct aaatcaactt taacgatgga tgatcttatg acacggggat ctttctttaa 2040
 agttcttaga atttcagact gtaccgcagc tgatgaatca aacagcatta aaaagtgata 2100
 tgctcgaaaa tgtttttcct ggtctttctt cattatttta ggaagatacc ttatgcccac 2160
 ggggtacaatg tccctcacca cacctctggt ttgaataatc agtttcccga ttgtggaaga 2220
 caattctttt gcttccaact ttggcgcatt ggagttgggt atgcgaacaa gtccgatcag 2280
 ctcataaagc atcttagtga aaagggtggt ttgctgttat tctttcctct gttgaagctt 2340

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met	Ala	Asn	Pro	Phe	Ser	Arg	Trp	Phe	Leu	Ser	Glu	Arg	Pro	Pro
1				5				10					15	
Asn	Cys	His	Val	Ala	Asp	Leu	Glu	Thr	Ser	Leu	Asp	Pro	His	Gln
				20				25					30	
Thr	Leu	Leu	Lys	Val	Gln	Lys	Tyr	Lys	Pro	Ala	Leu	Ser	Asp	Trp
								35						

35	40	45
Val His Tyr Ile Phe Leu Gly Ser Ile Met Leu Phe Val Phe Ile		
50	55	60
Thr Asn Pro Ala Pro Trp Ile Phe Lys Ile Leu Phe Tyr Cys Phe		
65	70	75
Leu Gly Thr Leu Phe Ile Ile Pro Ala Thr Ser Gln Phe Phe Phe		
80	85	90
Asn Ala Leu Pro Ile Leu Thr Trp Val Ala Leu Tyr Phe Thr Ser		
95	100	105
Ser Tyr Phe Pro Asp Asp Arg Arg Pro Pro Ile Thr Val Lys Val		
110	115	120
Leu Pro Ala Val Glu Thr Ile Leu Tyr Gly Asp Asn Leu Ser Asp		
125	130	135
Ile Leu Ala Thr Ser Thr Asn Ser Phe Leu Asp Ile Leu Ala Trp		
140	145	150
Leu Pro Tyr Gly Leu Phe His Tyr Gly Ala Pro Phe Val Val Ala		
155	160	165
Ala Ile Leu Phe Val Phe Gly Pro Pro Thr Val Leu Gln Gly Tyr		
170	175	180
Ala Phe Ala Phe Gly Tyr Met Asn Leu Phe Gly Val Ile Met Gln		
185	190	195
Asn Val Phe Pro Ala Ala Pro Pro Trp Tyr Lys Ile Leu Tyr Gly		
200	205	210
Leu Gln Ser Ala Asn Tyr Asp Met His Gly Ser Pro Gly Gly Leu		
215	220	225
Ala Arg Ile Asp Lys Leu Leu Gly Ile Asn Met Tyr Thr Thr Ala		
230	235	240
Phe Ser Asn Ser Ser Val Ile Phe Gly Ala Phe Pro Ser Leu His		
245	250	255
Ser Gly Cys Ala Thr Met Glu Ala Leu Phe Phe Cys Tyr Cys Phe		
260	265	270
Pro Lys Leu Lys Pro Leu Phe Ile Ala Tyr Val Cys Trp Leu Trp		

275	280	285
Trp Ser Thr Met Tyr Leu Thr His His Tyr Phe Val Asp Leu Met		
290	295	300
Ala Gly Ser Val Leu Ser Tyr Val Ile Phe Gln Tyr Thr Lys Tyr		
305	310	315
Thr His Leu Pro Ile Val Asp Thr Ser Leu Phe Cys Arg Trp Ser		
320	325	330
Tyr Thr Ser Ile Glu Lys Tyr Asp Ile Ser Lys Ser Asp Pro Leu		
335	340	345
Ala Ala Asp Ser Asn Asp Ile Glu Ser Val Pro Leu Ser Asn Leu		
350	355	360
Glu Leu Asp Phe Asp Leu Asn Met Thr Asp Glu Pro Ser Val Ser		
365	370	375
Pro Ser Leu Phe Asp Gly Ser Thr Ser Val Ser Arg Ser Ser Ala		
380	385	390
Thr Ser Ile Thr Ser Leu Gly Val Lys Arg Ala		
395	400	

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

tttctttctg tcaaagaata ataaagtgcc catcagtgtt catatttggtt acaaagtggg 60
tttctgattt ggtactactg cagaggcgta ttttttgctt cagttaccat agcgtaagaa 120
cactagcgac ttttgttcgt gaaccaacag agtaggattt ctactgctac atctcttagg 180
tagttggtta gtccgatcgc tcacttttgg ttgttggttaa gtacttcata agtttatcct 240
tttccttttt cacactgagc tactttgggt atagcttttg gcccaaggat ctttgaattt 300

```

tctccaaaag tactttattht tatatcttac aggtttgcggt tttcatattht taaaaagctt 360
tttaatcatt cctttgcgta tggcaaacc cttttcgaga tggtttctat cagagagacc 420
tccaaactgc catgtagccg atttagaaac aagtttagat ccccatcaaa cgttggttgaa 480
ggtgcaaaaa tacaaaccg ctttaagcga ctgggtgcat tacatcttct tgggatccat 540
catgctgttt gtgttcatta ctaatccgc accttgatc ttcaagatcc ttttttattg 600
tttcttgggc actttattca tcattccagc tacgtcacag tttttcttca atgccttgcc 660
catcctaaca tgggtggcgc tgtatttcac ttcacgtac tttccagatg accgcaggcc 720
tcctattact gtcaaagtgt taccagcggg ggaacaatt ttatacggcg acaatttaag 780
tgatattctt gcaacatcga cgaattcctt tttggacatt ttagcatggt taccgtacgg 840
actatttcat tttggggccc catttgctgt tgctgccatc ttattcgtat ttggtccacc 900
aactgttttg caaggttatg cttttgcatt tggttatatg aacctgtttg gtgttatcat 960
gcaaatgtc tttccagccg ctcccccag gtataaaatt ctctatggat tgcaatcagc 1020
caactatgat atgcatggct cgcttgggtg attagctaga attgataagc tactcggtat 1080
taatattgat actacagctt tttcaaattc ctccgtcatt ttcggtgctt ttccttcact 1140
gcattccggg tgtgctacta tggaaagccct gtttttctgt tattgttttc caaaattgaa 1200
gcccttgtht attgcttatg tttgctgggt atgggtggta actatgtatc tgacacacca 1260
ttattttgta gaccttatgg caggttctgt gctgtcatac gttattttcc agtacacaaa 1320
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tgagaaatac gatatatcaa agagtgatcc attggctgca gattcaaagc atatcgaaag 1440
tgtcccttg tccaacttg aacttgactt tgatcttaat atgactgatg aaccagtggt 1500
aagcccttcg ttatttgatg gatctacttc tgtttctcgt tcgtccgcca cgtctataac 1560
gtcactaggt gtaaagagg cttaatgagt attttatctg caattacgga tacggttggt 1620
cttatgtaga tacatataaa tatatatctt tttctttctt tttcttagtc aggattgtcg 1680
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aatgctcttc ctgctthgtt tattatatgt gtatgaaaga tatgtatgta tttacatgtg 1860
ttttagcgt cccagtc aaacctgtgc ctatacctaa atggattgat aatcttcatt 1920
cactaattct aaaatagact tcttcccaa agaacgggtg aacgatgagg ctctatccag 1980
ctgcttatct aaatcaactt taacgatgga tgatcttatg acacggggat ctttctthta 2040
agttcttaga atttcagact gtaccgcagc tgatgaatca aacagcatta aaaagtgata 2100
tgctcgaaaa tgtttttcct ggtctttctt cattattthta ggaagatacc ttatgccccat 2160
gggtacaatg tccctacca cacctctgtt ttgaataatc agtttcccg tttgtggaaga 2220

caattctttt gcttccaact ttggcgcat tggagttggtt atgcgaacaa gtccgatcag 2280
ctcataaagc atcttagtga aaaggggtggt tttgcgttat tctttcctct gttgaagctt 2340

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met	Ala	Asn	Pro	Phe	Ser	Arg	Trp	Phe	Leu	Ser	Glu	Arg	Pro	Pro
1				5					10					15
Asn	Cys	His	Val	Ala	Asp	Leu	Glu	Thr	Ser	Leu	Asp	Pro	His	Gln
				20					25					30
Thr	Leu	Leu	Lys	Val	Gln	Lys	Tyr	Lys	Pro	Ala	Leu	Ser	Asp	Trp
				35					40					45
Val	His	Tyr	Ile	Phe	Leu	Gly	Ser	Ile	Met	Leu	Phe	Val	Phe	Ile
				50					55					60
Thr	Asn	Pro	Ala	Pro	Trp	Ile	Phe	Lys	Ile	Leu	Phe	Tyr	Cys	Phe
				65					70					75
Leu	Gly	Thr	Leu	Phe	Ile	Ile	Pro	Ala	Thr	Ser	Gln	Phe	Phe	Phe
				80					85					90
Asn	Ala	Leu	Pro	Ile	Leu	Thr	Trp	Val	Ala	Leu	Tyr	Phe	Thr	Ser
				95					100					105
Ser	Tyr	Phe	Pro	Asp	Asp	Arg	Arg	Pro	Pro	Ile	Thr	Val	Lys	Val
				110					115					120
Leu	Pro	Ala	Val	Glu	Thr	Ile	Leu	Tyr	Gly	Asp	Asn	Leu	Ser	Asp
				125					130					135
Ile	Leu	Ala	Thr	Ser	Thr	Asn	Ser	Phe	Leu	Asp	Ile	Leu	Ala	Trp
				140					145					150

Leu Pro Tyr Gly	Leu Phe His Phe Gly	Ala Pro Phe Val Val	Ala
155	160	165	
Ala Ile Leu Phe	Val Phe Gly Pro Pro	Thr Val Leu Gln Gly	Tyr
170	175	180	
Ala Phe Ala Phe	Gly Tyr Met Asn Leu	Phe Gly Val Ile Met	Gln
185	190	195	
Asn Val Phe Pro	Ala Ala Pro Pro Trp	Tyr Lys Ile Leu Tyr	Gly
200	205	210	
Leu Gln Ser Ala	Asn Tyr Asp Met His	Gly Ser Pro Gly Gly	Leu
215	220	225	
Ala Arg Ile Asp	Lys Leu Leu Gly Ile	Asn Met Tyr Thr Thr	Ala
230	235	240	
Phe Ser Asn Ser	Ser Val Ile Phe Gly	Ala Phe Pro Ser Leu	His
245	250	255	
Ser Gly Cys Ala	Thr Met Glu Ala Leu	Phe Phe Cys Tyr Cys	Phe
260	265	270	
Pro Lys Leu Lys	Pro Leu Phe Ile Ala	Tyr Val Cys Trp Leu	Trp
275	280	285	
Trp Ser Thr Met	Tyr Leu Thr His His	Tyr Phe Val Asp Leu	Met
290	295	300	
Ala Gly Ser Val	Leu Ser Tyr Val Ile	Phe Gln Tyr Thr Lys	Tyr
305	310	315	
Thr His Leu Pro	Ile Val Asp Thr Ser	Leu Phe Cys Arg Trp	Ser
320	325	330	
Tyr Thr Ser Ile	Glu Lys Tyr Asp Ile	Ser Lys Ser Asp Pro	Leu
335	340	345	
Ala Ala Asp Ser	Asn Asp Ile Glu Ser	Val Pro Leu Ser Asn	Leu
350	355	360	
Glu Leu Asp Phe	Asp Leu Asn Met Thr	Asp Glu Pro Ser Val	Ser
365	370	375	
Pro Ser Leu Phe	Asp Gly Ser Thr Ser	Val Ser Arg Ser Ser	Ala
380	385	390	

Thr Ser Ile Thr Ser Leu Gly Val Lys Arg Ala

395

400

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5340 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```
agcgcttcta ttttctccc caccgcgagg cggaaatggc acattttttt tcttttgctt 60
ctgtgctttt gctgtaattt ttggcatgtg ctattgtatg aagataacgc gtggttccgt 120
ggaaatagcc ggaaattttg ccgggaatat gacggacatg atttaacacc cgtggaaatg 180
aaaaaagcca aggtaagaaa gtggcaatat ttttctaca aatagatctg ctgtccctta 240
gatgattacc atacatatat atatttatta cacacatctg tcagaggtag ctagcgaagg 300
tgtcactgaa atattttttg ttccagttag tataaatacg gaggtagaac agctctccgc 360
gtgtatatct ttttttgcg cgtacagaag caggaagaac gcatttccat acctttttct 420
ccttacaggt gccctctgag tagtgtcacg aacgaggaaa aagattaata ttactgtttt 480
tatattcaaa aagagtaaag ccgttgctat atacgaatat gacgattacc gtgggggatg 540
cagtttcgga gacggagctg gaaaacaaaa gtcaaaacgt ggtactatct cccaaggcat 600
ctgcttcttc agacataagc acagatgttg ataaagacac atcgtcttct tgggatgaca 660
aatctttgct gcctacaggt gaatatattg tggacagaaa taagcccaa acctacttga 720
atagcgatga tatcgaaaaa gtgacagaat ctgatatttt ccctcagaaa cgtctgtttt 780
cattcttgca ctctaagaaa attccagaag taccacaaac cgatgacgag aggaagatat 840
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ccaaactacc taaacatata gttctgagag ctttattatt cacttttaag aaacagtact 1140
tcatgtcgat agtgtttgca attctcgcta attgtacatc cggttttaac cccatgatta 1200
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ccaagaggct aattgagttt gtcgaagaaa aggctatttt tcatagcatg catgttaaca 1260
 aaggtattgg ttacgctatt ggtgcatggt tgatgatggt cgttaacggg ttgacgttca 1320
 atcatttctt tcatacatcc caactgactg gtgtgcaagc taagtctatt cttactaaag 1380
 ctgccatgaa gaaaatgttt aatgcatcta attatgcgag acattgtttt cctaacggta 1440
 aagtgacttc ttttgtaaca acagatctcg ctagaattga atttgcctta tcttttcagc 1500
 cgtttttggc tgggttcctt gcaattttgg ctatttgcag tgttttattg atcgtaacc 1560
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 tctcttctca aaattcggag aaagaggatg aagaacagga agcggttggt tccggtgaat 3000
 tgggacaact aaaatatgaa ccagaggtaa aggaattgac tgaactgaag aaaaaggcta 3060
 cagaaatgtc acaaactgca aatagtggta aaattgtagc ggatgggtcat actagtagta 3120

aagaagaaag agcagtcaat agtatcagtc tgaaaatata ccgtgaatac attaaagctg 3180
cagtaggtaa gtgggggtttt atcgccactac cggtgtatgc aatttttagtc gttggaacca 3240
cattctgctc acttttttct tccgtttggt tatcttactg gactgagaat aaattcaaaa 3300
acagaccacc cagtttttat atgggtcttt actccttctt tgtgtttgct gctttcatat 3360
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gaagtcagga acgatttttg gcgaaatcag attttttgat caacaagatg aatgaggcgg 3840
gataccttgt agttgtcctg caaagatggg taggtatttt cttgatatg gttgctatcg 3900
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ctatgacttg cagaaaaagt tatgtgtgcc atagatagat ataattgcat acccacatcg 5100
tataactcaa attccgaaaa gaacatttca ttttttatga ggcaaactga acaacgcttc 5160
ggtccttttt tcattctaga aatatatatt tatacatcat tttcagaaga tattcaaaga 5220
acttattggg atgtctatct actgaataaa gtatacacia aaaacgaatt taaaatggaa 5280
ggcataaata gaaaacttag aagtgaaaat cctaaaaccg aaggatattt caaatacgta 5340

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1477 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met	Thr	Ile	Thr	Val	Gly	Asp	Ala	Val	Ser	Glu	Thr	Glu	Leu	Glu
				5					10					15
Asn	Lys	Ser	Gln	Asn	Val	Val	Leu	Ser	Pro	Lys	Ala	Ser	Ala	Ser
				20					25					30
Ser	Asp	Ile	Ser	Thr	Asp	Val	Asp	Lys	Asp	Thr	Ser	Ser	Ser	Trp
				35					40					45
Asp	Asp	Lys	Ser	Leu	Leu	Pro	Thr	Gly	Glu	Tyr	Ile	Val	Asp	Arg
				50					55					60
Asn	Lys	Pro	Gln	Thr	Tyr	Leu	Asn	Ser	Asp	Asp	Ile	Glu	Lys	Val
				65					70					75
Thr	Glu	Ser	Asp	Ile	Phe	Pro	Gln	Lys	Arg	Leu	Phe	Ser	Phe	Leu
				80					85					90
His	Ser	Lys	Lys	Ile	Pro	Glu	Val	Pro	Gln	Thr	Asp	Asp	Glu	Arg
				95					100					105
Lys	Ile	Tyr	Pro	Leu	Phe	His	Thr	Asn	Ile	Ile	Ser	Asn	Met	Phe
				110					115					120
Phe	Trp	Trp	Val	Leu	Pro	Ile	Leu	Arg	Val	Gly	Tyr	Lys	Arg	Thr

125	130	135
Ile Gln Pro Asn Asp Leu Phe Lys Met	Asp Pro Arg Met Ser Ile	
140	145	150
Glu Thr Leu Tyr Asp Asp Phe Glu Lys	Asn Met Ile Tyr Tyr Phe	
155	160	165
Glu Lys Thr Arg Lys Lys Tyr Arg Lys	Arg His Pro Glu Ala Thr	
170	175	180
Glu Glu Glu Val Met Glu Asn Ala Lys	Leu Pro Lys His Thr Val	
185	190	195
Leu Arg Ala Leu Leu Phe Thr Phe Lys	Lys Gln Tyr Phe Met Ser	
200	205	210
Ile Val Phe Ala Ile Leu Ala Asn Cys	Thr Ser Gly Phe Asn Pro	
215	220	225
Met Ile Thr Lys Arg Leu Ile Glu Phe	Val Glu Glu Lys Ala Ile	
230	235	240
Phe His Ser Met His Val Asn Lys Gly	Ile Gly Tyr Ala Ile Gly	
245	250	255
Ala Cys Leu Met Met Phe Val Asn Gly	Leu Thr Phe Asn His Phe	
260	265	270
Phe His Thr Ser Gln Leu Thr Gly Val	Gln Ala Lys Ser Ile Leu	
275	280	285
Thr Lys Ala Ala Met Lys Lys Met Phe	Asn Ala Ser Asn Tyr Ala	
290	295	300
Arg His Cys Phe Pro Asn Gly Lys Val	Thr Ser Phe Val Thr Thr	
305	310	315
Asp Leu Ala Arg Ile Glu Phe Ala Leu	Ser Phe Gln Pro Phe Leu	
320	325	330
Ala Gly Phe Pro Ala Ile Leu Ala Ile	Cys Ile Val Leu Leu Ile	
335	340	345
Val Asn Leu Gly Pro Ile Ala Leu Val	Gly Ile Gly Ile Phe Phe	
350	355	360
Gly Gly Phe Phe Ile Ser Leu Phe Ala	Phe Lys Leu Ile Leu Gly	

365	370	375
Phe Arg Ile Ala	Ala Asn Ile Phe Thr Asp Ala Arg Val Thr Met	
380	385	390
Met Arg Glu Val	Leu Asn Asn Ile Lys Met Ile Lys Tyr Tyr Thr	
395	400	405
Trp Glu Asp Ala	Tyr Glu Lys Asn Ile Gln Asp Ile Arg Thr Lys	
410	415	420
Glu Ile Ser Lys	Val Arg Lys Met Gln Leu Ser Arg Asn Phe Leu	
425	430	435
Ile Ala Met Ala	Met Ser Leu Pro Ser Ile Ala Ser Leu Val Thr	
440	445	450
Phe Leu Ala Met	Tyr Lys Val Asn Lys Gly Gly Arg Gln Pro Gly	
455	460	465
Asn Ile Phe Ala	Ser Leu Ser Leu Phe Gln Val Leu Ser Leu Gln	
470	475	480
Met Phe Phe Leu	Pro Ile Ala Ile Gly Thr Gly Ile Asp Met Ile	
485	490	495
Ile Gly Leu Gly	Arg Leu Gln Ser Leu Leu Glu Ala Pro Glu Asp	
500	505	510
Asp Pro Asn Gln	Met Ile Glu Met Lys Pro Ser Pro Gly Phe Asp	
515	520	525
Pro Lys Leu Ala	Leu Lys Met Thr His Cys Ser Phe Glu Trp Glu	
530	535	540
Asp Tyr Glu Leu	Asn Asp Ala Ile Glu Glu Ala Lys Gly Glu Ala	
545	550	555
Lys Asp Glu Gly	Lys Lys Asn Lys Lys Lys Arg Lys Asp Thr Trp	
560	565	570
Gly Lys Pro Ser	Ala Ser Thr Asn Lys Ala Lys Arg Leu Asp Asn	
575	580	585
Met Leu Lys Asp	Arg Asp Gly Pro Glu Asp Leu Glu Lys Thr Ser	
590	595	600
Phe Arg Gly Phe	Lys Asp Leu Asn Phe Asp Ile Lys Lys Gly Glu	

605	610	615
Phe Ile Met Ile Thr Gly Pro Ile Gly Thr Gly Lys Ser Ser Leu		
620	625	630
Leu Asn Ala Met Ala Gly Ser Met Arg Lys Ile Asp Gly Lys Val		
635	640	645
Glu Val Asn Gly Asp Leu Leu Met Cys Gly Tyr Pro Trp Ile Gln		
650	655	660
Asn Ala Ser Val Arg Asp Asn Ile Ile Phe Gly Ser Pro Phe Asn		
665	670	675
Lys Glu Lys Tyr Asp Glu Val Val Arg Val Cys Ser Leu Lys Ala		
680	685	690
Asp Leu Asp Ile Leu Pro Ala Gly Asp Met Thr Glu Ile Gly Glu		
695	700	705
Arg Gly Ile Thr Leu Ser Gly Gly Gln Lys Ala Arg Ile Asn Leu		
710	715	720
Ala Arg Ser Val Tyr Lys Lys Lys Asp Ile Tyr Val Phe Asp Asp		
725	730	735
Val Leu Ser Ala Val Asp Ser Arg Val Gly Lys His Ile Met Asp		
740	745	750
Glu Cys Leu Thr Gly Met Leu Ala Asn Lys Thr Arg Ile Leu Ala		
755	760	765
Thr His Gln Leu Ser Leu Ile Glu Arg Ala Ser Arg Val Ile Val		
770	775	780
Leu Gly Thr Asp Gly Gln Val Asp Ile Gly Thr Val Asp Glu Leu		
785	790	795
Lys Ala Arg Asn Gln Thr Leu Ile Asn Leu Leu Gln Phe Ser Ser		
800	805	810
Gln Asn Ser Glu Lys Glu Asp Glu Glu Gln Glu Ala Val Val Ser		
815	820	825
Gly Glu Leu Gly Gln Leu Lys Tyr Glu Pro Glu Val Lys Glu Leu		
830	835	840
Thr Glu Leu Lys Lys Lys Ala Thr Glu Met Ser Gln Thr Ala Asn		

845	850	855
Ser Gly Lys Ile Val Ala Asp Gly His Thr Ser Ser Lys Glu Glu		
860	865	870
Arg Ala Val Asn Ser Ile Ser Leu Lys Ile Tyr Arg Glu Tyr Ile		
875	880	885
Lys Ala Ala Val Gly Lys Trp Gly Phe Ile Ala Leu Pro Leu Tyr		
890	895	900
Ala Ile Leu Val Val Gly Thr Thr Phe Cys Ser Leu Phe Ser Ser		
905	910	915
Val Trp Leu Ser Tyr Trp Thr Glu Asn Lys Phe Lys Asn Arg Pro		
920	925	930
Pro Ser Phe Tyr Met Gly Leu Tyr Ser Phe Phe Val Phe Ala Ala		
935	940	945
Phe Ile Phe Met Asn Gly Gln Phe Thr Ile Leu Cys Ala Met Gly		
950	955	960
Ile Met Ala Ser Lys Trp Leu Asn Leu Arg Ala Val Lys Arg Ile		
965	970	975
Leu His Thr Pro Met Ser Tyr Ile Asp Thr Thr Pro Leu Gly Arg		
980	985	990
Ile Leu Asn Arg Phe Thr Lys Asp Thr Asp Ser Leu Asp Asn Glu		
995	1000	1005
Leu Thr Glu Ser Leu Arg Leu Met Thr Ser Gln Phe Ala Asn Ile		
1010	1015	1020
Val Gly Val Cys Val Met Cys Ile Val Tyr Leu Pro Trp Phe Ala		
1025	1030	1035
Ile Ala Ile Pro Phe Leu Leu Val Ile Phe Val Leu Ile Ala Asp		
1040	1045	1050
His Tyr Gln Ser Ser Gly Arg Glu Ile Lys Arg Leu Glu Ala Val		
1055	1060	1065
Gln Arg Ser Phe Val Tyr Asn Asn Leu Asn Glu Val Leu Gly Gly		
1070	1075	1080
Met Asp Thr Ile Lys Ala Tyr Arg Ser Gln Glu Arg Phe Leu Ala		

1085	1090	1095
Lys Ser Asp Phe Leu Ile Asn Lys Met Asn Glu Ala Gly Tyr Leu		
1100	1105	1110
Val Val Val Leu Gln Arg Trp Val Gly Ile Phe Leu Asp Met Val		
1115	1120	1125
Ala Ile Ala Phe Ala Leu Ile Ile Thr Leu Leu Cys Val Thr Arg		
1130	1135	1140
Ala Phe Pro Ile Ser Ala Ala Ser Val Gly Val Leu Leu Thr Tyr		
1145	1150	1155
Val Leu Gln Leu Pro Gly Leu Leu Asn Thr Ile Leu Arg Ala Met		
1160	1165	1170
Thr Gln Thr Glu Asn Asp Met Asn Ser Ala Glu Arg Leu Val Thr		
1175	1180	1185
Tyr Ala Thr Glu Leu Pro Leu Glu Ala Ser Tyr Arg Lys Pro Glu		
1190	1195	1200
Met Thr Pro Pro Glu Ser Trp Pro Ser Met Gly Glu Ile Ile Phe		
1205	1210	1215
Glu Asn Val Asp Phe Ala Tyr Arg Pro Gly Leu Pro Ile Val Leu		
1220	1225	1230
Lys Asn Leu Asn Leu Asn Ile Lys Ser Gly Glu Lys Ile Gly Ile		
1235	1240	1245
Cys Gly Arg Thr Gly Ala Gly Lys Ser Thr Ile Met Ser Ala Leu		
1250	1255	1260
Tyr Arg Leu Asn Glu Leu Thr Ala Gly Lys Ile Leu Ile Asp Asn		
1265	1270	1275
Val Asp Ile Ser Gln Leu Gly Leu Phe Asp Leu Arg Arg Lys Leu		
1280	1285	1290
Ala Ile Ile Pro Gln Asp Pro Val Leu Phe Arg Gly Thr Ile Arg		
1295	1300	1305
Lys Asn Leu Asp Pro Phe Asn Glu Arg Thr Asp Asp Glu Leu Trp		
1310	1315	1320
Asp Ala Leu Val Arg Gly Gly Ala Ile Ala Lys Asp Asp Leu Pro		

1325	1330	1335
Glu Val Lys Leu Gln Lys Pro Asp Glu Asn Gly Thr His Gly Lys		
1340	1345	1350
Met His Lys Phe His Leu Asp Gln Ala Val Glu Glu Glu Gly Ser		
1355	1360	1365
Asn Phe Ser Leu Gly Glu Arg Gln Leu Leu Ala Leu Thr Arg Ala		
1370	1375	1380
Leu Val Arg Gln Ser Lys Ile Leu Ile Leu Asp Glu Ala Thr Ser		
1385	1390	1395
Ser Val Asp Tyr Glu Thr Asp Gly Lys Ile Gln Thr Arg Ile Val		
1400	1405	1410
Glu Glu Phe Gly Asp Cys Thr Ile Leu Cys Ile Ala His Arg Leu		
1415	1420	1425
Lys Thr Ile Val Asn Tyr Asp Arg Ile Leu Val Leu Glu Lys Gly		
1430	1435	1440
Glu Val Ala Glu Phe Asp Thr Pro Trp Thr Leu Phe Ser Gln Glu		
1445	1450	1455
Asp Ser Ile Phe Arg Ser Met Cys Ser Arg Ser Gly Ile Val Glu		
1460	1465	1470
Asn Asp Phe Glu Asn Arg Ser		
1475		

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid (synthetic DNA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

tttggttaya tgaayytntt yggngt 26

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid (synthetic DNA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

tctacaaart artggtgngt narrtacat 29

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2274 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```
ttatatatat tattgatttg ttcctgttgt tatttagttt agaatcagac gactacacca 60
gaaccacaat tcaaccaaca cttatataga acctggcttg gaaaaaagta acatttatca 120
ttcctatact tttttagcaa acataatccg tgttttacat atattattca cccaatatca 180
taacaaaaac aaactgaata atggcgtcct ctattttgcg ttccaaaata atacaaaaac 240
cgtaccaatt attccactac tattttcttc tggagaaggc tcctggttct acagttagtg 300
atgtgaattt tgatacaaac atacaaacga gtttacgtaa attaaagcat catcattgga 360
cgggtgggaga aatattccat tatggggttt tggtttccat actttttttc gtgtttgtgg 420
ttttcccagc ttcatttttt ataaaattac caataatcct agcatttgct acttgttttt 480
taataccctt aacatcacaa ttttttcttc ctgccttgcc cgttttcact tggttggcat 540
tatattttac gtgtgctaaa atacctcaag aatggaaacc agctatcaca gttaaagttt 600
taccagctat ggaaacaatt ttgtacggcg ataatttatc aaatgttttg gcaaccatca 660
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ctaccggagt gttagatata ttggcatggt taccatatgg gattattcat ttcagtttcc 720
catttgact tgctgctatt atatTTTTat ttgggccacc gacggcatta agatcatttg 780
gatttgcctt tggttatatg aacttgcttg gagtcttgat tcaaatggca ttcccagctg 840
ctcctccatg gtacaaaaac ttgcacggat tagaaccagc taattattca atgcacgggt 900
ctcctggtgg acttgaaggg atagataaat tgttaggtgt tgatatgtat accacagggg 960
tttccaattc atcaatcatt tttggggcat tcccatcgtt acattcagga tgttgatatca 1020
tggaagtgtt atttttgtgt tggttgtttc cacgattcaa gtttggtgtg gttacatacg 1080
catcttggct ttggtggagc acgatgtatt tgacctatca ctactttgtc gatttgattg 1140
gtggagccat gctatctttg actgtttttg agttcaccaa atataaatat ttgccaaaaa 1200
acaaagaagg ctttttctgt cgttgggtcat aactgaaat tgaaaaaatc gatatccaag 1260
agattgacc tttatcatac aattatatcc ctgtcaacag caatgataat gaaagcagat 1320
tgtatacgag agtgtaccaa gagtctcagg ttagtcccc acagagagct gaaacacctg 1380
aagcatttga gatgtcaaat ttttctaggt ctagacaaag ctcaaagact caggttccat 1440
tgagtaatct tactaacaat gatcaagtgt ctggaattaa cgaagaggat gaagaagaag 1500
aaggcgatga aatttcacg agtactcctt cgggtgttga agacgaacca cagggtagca 1560
catatgctgc atcctcagct acatcagtag atgatttggg ttccaaaaga aattagtaaa 1620
ataacagttt ctattaattt ctttatttcc tcctaattaa tgattttatg ctcaatacct 1680
acactatctg tttttaattt cctacttttt ttttattatt gttgagttca tttgctgttc 1740
attgaatatt tacaattttg cattaattac catcaatata gaatgggcac agttttttta 1800
agtttttttg ttttgtgtt tgtctttctt tttttacatt aatgtgtttg gattgtttta 1860
ggttccttta tcccttagcc ccctcagaat actattttat ctaattaatt tgtttttatt 1920
ttctgatatt taccaattgc ttttctttt ggatatttat aatagcatcc cctaataatt 1980
aatatacaac tgtttcatat atatacgtgt atgtcctgta gtggtggaaa ctggagtcaa 2040
catttgattt aatgtgtaca agaaagcagt gttaatgcta ctattataat ttttgaggtg 2100
caaatcaaga ggttggcagc tttcttatgg ctatgaccgt gaatgaaggc ttgtaaacca 2160
cgtaataaac aaaagccaac aagttttttt agagccttta acaacatacg caatgagagt 2220
gattgcaata ctacaagata tagcccaaaa aattgaatgc atttcaacaa caac 2274

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(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met	Ala	Ser	Ser	Ile	Leu	Arg	Ser	Lys	Ile	Ile	Gln	Lys	Pro	Tyr
				5					10					15
Gln	Leu	Phe	His	Tyr	Tyr	Phe	Leu	Ser	Glu	Lys	Ala	Pro	Gly	Ser
				20					25					30
Thr	Val	Ser	Asp	Leu	Asn	Phe	Asp	Thr	Asn	Ile	Gln	Thr	Ser	Leu
				35					40					45
Arg	Lys	Leu	Lys	His	His	His	Trp	Thr	Val	Gly	Glu	Ile	Phe	His
				50					55					60
Tyr	Gly	Phe	Leu	Val	Ser	Ile	Leu	Phe	Phe	Val	Phe	Val	Val	Phe
				65					70					75
Pro	Ala	Ser	Phe	Phe	Ile	Lys	Leu	Pro	Ile	Ile	Leu	Ala	Phe	Ala
				80					85					90
Thr	Cys	Phe	Leu	Ile	Pro	Leu	Thr	Ser	Gln	Phe	Phe	Leu	Pro	Ala
				95					100					105
Leu	Pro	Val	Phe	Thr	Trp	Leu	Ala	Leu	Tyr	Phe	Thr	Cys	Ala	Lys
				110					115					120
Ile	Pro	Gln	Glu	Trp	Lys	Pro	Ala	Ile	Thr	Val	Lys	Val	Leu	Pro
				125					130					135
Ala	Met	Glu	Thr	Ile	Leu	Tyr	Gly	Asp	Asn	Leu	Ser	Asn	Val	Leu
				140					145					150
Ala	Thr	Ile	Thr	Thr	Gly	Val	Leu	Asp	Ile	Leu	Ala	Trp	Leu	Pro
				155					160					165
Tyr	Gly	Ile	Ile	His	Phe	Ser	Phe	Pro	Phe	Val	Leu	Ala	Ala	Ile
				170					175					180
Ile	Phe	Leu	Phe	Gly	Pro	Pro	Thr	Ala	Leu	Arg	Ser	Phe	Gly	Phe
				185					190					195
Ala	Phe	Gly	Tyr	Met	Asn	Leu	Leu	Gly	Val	Leu	Ile	Gln	Met	Ala

200	205	210
Phe Pro Ala Ala Pro Pro Trp Tyr Lys	Asn Leu His Gly Leu Glu	
215	220	225
Pro Ala Asn Tyr Ser Met His Gly Ser	Pro Gly Gly Leu Gly Arg	
230	235	240
Ile Asp Lys Leu Leu Gly Val Asp Met	Tyr Thr Thr Gly Phe Ser	
245	250	255
Asn Ser Ser Ile Ile Phe Gly Ala Phe	Pro Ser Leu His Ser Gly	
260	265	270
Cys Cys Ile Met Glu Val Leu Phe Leu	Cys Trp Leu Phe Pro Arg	
275	280	285
Phe Lys Phe Val Trp Val Thr Tyr Ala	Ser Trp Leu Trp Trp Ser	
290	295	300
Thr Met Tyr Leu Thr His His Tyr Phe	Val Asp Leu Ile Gly Gly	
305	310	315
Ala Met Leu Ser Leu Thr Val Phe Glu	Phe Thr Lys Tyr Lys Tyr	
320	325	330
Leu Pro Lys Asn Lys Glu Gly Leu Phe	Cys Arg Trp Ser Tyr Thr	
335	340	345
Glu Ile Glu Lys Ile Asp Ile Gln Glu	Ile Asp Pro Leu Ser Tyr	
350	355	360
Asn Tyr Ile Pro Val Asn Ser Asn Asp	Asn Glu Ser Arg Leu Tyr	
365	370	375
Thr Arg Val Tyr Gln Glu Ser Gln Val	Ser Pro Pro Gln Arg Ala	
380	385	390
Glu Thr Pro Glu Ala Phe Glu Met Ser	Asn Phe Ser Arg Ser Arg	
395	400	405
Gln Ser Ser Lys Thr Gln Val Pro Leu	Ser Asn Leu Thr Asn Asn	
410	415	420
Asp Gln Val Ser Gly Ile Asn Glu Glu	Asp Glu Glu Glu Glu Gly	
425	430	435
Asp Glu Ile Ser Ser Ser Thr Pro Ser	Val Phe Glu Asp Glu Pro	

440	445	450
Gln Gly Ser Thr Tyr Ala Ala Ser Ser	Ala Thr Ser Val Asp Asp	
455	460	465
Leu Asp Ser Lys Arg Asn		
470		

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```

tttgaaaaat ttgaatttta aaattaatcc aatggaaaaa attggtatTT gtggaagaac 60
cggtgctggt aaatcatcaa ttatgacagc attatatcga ttatcagaat tagaactggg 120
gaaaattatt attgatgata ttgatatttc aactttgggt ttaaaagatc ttcgatcaaa 180
attatcaatt attcctcaag atccagtatt attccgaggt tcaattcgga aaaacttgga 240
tcc 243

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(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Leu Lys Asn Leu Asn Phe Lys Ile Asn Pro Met Glu Lys Ile Gly
5 10 15
55

Ile Cys Gly Arg Thr Gly Ala Gly Lys Ser Ser Ile Met Thr Ala		
	20	25
Leu Tyr Arg Leu Ser Glu Leu Glu Leu Gly Lys Ile Ile Ile Asp		30
	35	40
Asp Ile Asp Ile Ser Thr Leu Gly Leu Lys Asp Leu Arg Ser Lys		45
	50	55
Leu Ser Ile Ile Pro Gln Asp Pro Val Leu Phe Arg Gly Ser Ile		60
	65	70
Arg Lys Asn Leu Asp		75
	80	

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1601 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iv) ANTI-SENSE: Yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

aggaagatga cttgcatcaa agatggagga agtgggtactg gcaggacgat caatcaaadc	60
agcagcagga ctaggtaacg gctcaggtga tgatgaaccc acggaccatt catgatcggc	120
gtagcaagt tccatattgt taagaccact catgaaggct actgcattag ggttttgagt	180
aaaagaatcc cttccaagta agtatgggct gccggtacga gccaaggagt tgctgggttt	240
ttcggaagaa ccatgaccgt ggataacaaa ctcgtattcc caacgaagga ttttaccagt	300
ttgcaactgt gggaggcgta gcttttgagc aaaaacgaag catataatag ctaaacacat	360
accgccgacc aaatctacaa agtagtggtg ggtaagggtac atagtacacc agcaaagcca	420
tagaacatat ccataaaagc agaagcggtg tcgaggaaac acatgcgaaa ggaaaagtgc	480
ttccagcatg gcccatccag cgtgaagaga tggaaaggca ccaaaaaaca ccggagagtt	540
agaaaaacca tcagtgtaaa tgctagtgcc gaagagagca tcaatacggg ccaatccacc	600
aggagagcca cgtactgcat acgtggcagg ttctaaacca tacatatttt cataccaagg	660

aggagaacag	gggaaagcca	tttggataag	aacaccaa	aaattcatat	aacaaaaagt	720
tcgagcccaa	actggaagag	ttccaggagg	tgcaaagatg	aaaagaataa	atgaaatgat	780
aaaaggagcc	gaataatgca	tgactccata	tggaacccag	gccaaaaatat	caaggatgct	840
atgcgtggtt	ttcgagagaa	gactagaaag	attagagcca	taaagaatat	tttcaagtgt	900
gggtaaaaaca	cgaacccata	tggttgacg	ccagcgttct	ggaataaacc	tacaagagta	960
aaataaaatt	gcccagggtga	tgataacaat	ggcaggaaaa	aaaatttggc	gtgttaaagg	1020
aacggtcaac	gcaatggcca	aaagacaggc	aatgccaaat	ttccccaga	atccaggaga	1080
ttcaatgaca	atacaagcaa	aatcaaatt	acctgctaga	aacacatatt	gcaaattgtgt	1140
ccatgaccat	ttcgtattgc	gtagcaaacg	aatgtaggc	atagggttta	agcttgtttc	1200
caacttgat	tggtatgctc	ggttacacgc	agcaaggcgc	ttttttaagg	tcgaaagagc	1260
agacattgct	tcaaagaatt	atcagagtaa	aaaaggaag	cgtacgaaaa	aaatttcgta	1320
aggaattaac	cggaaaacta	aaggaaaaaa	aaggaatttt	tatgaaggaa	agaaagtagc	1380
tattaaatgc	aagtgtcaag	cacttaaaag	tagcgatgta	aaatatttaa	aaaaagatgg	1440
accgattaac	caatgttcag	ctcacagttg	ccagcaatca	gggctatttt	tttatttttt	1500
ttataaaatt	gctaattata	tataatataa	ttagtttatt	aacttgcttt	tcctcaaaaa	1560
accaattcga	gaaaggaact	tttgagagg	caaaaaagct	t		1601

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1601 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: mRNA

(iv) ANTI-SENSE: Yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

aggaagauga	cuugcaucaa	agauggagga	agugguacug	gcaggacgau	caaucaaauc	60
agcagcagga	cuagguaacg	gcucagguga	ugaugaaccc	acggaccuuu	caugaucggu	120
guuagcaagu	uccauauugu	uaagaccacu	caugaaggcu	acugcauuag	gguuuugagu	180
aaaagaaucc	cuuccaagua	aguaugggcu	gccgguacga	gccaaggagu	ugcugguuuu	240
uucggaaaga	ccaugaccgu	ggauaacaaa	cucguauucc	caacgaagga	uuuuaccagu	300

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uugcaacugu gggaggcgua gcuuuugagc aaaaacgaag cauauauag cuaaacacau 360
accgccgacc aaauacuaca aguaguggug gguaagguac auaguacacc agcaaagcca 420
uagaacauau ccuaaaaagc agaagcggua ucgaggaaac acaugcgaaa ggaaaagugc 480
uuccagcaug gcccauccag cgugaagaga uggaaaggca ccaaaaacaa ccggagaguu 540
agaaaaacca ucaguguaaa ugcuaugucc gaagagagca ucaauacggg ccaauccacc 600
aggagagcca cguacugcau acguggcagg uucuaaacca uacauauuuu cauaccaagg 660
aggagaacag gggaaagcca uuuggauaag aacaccaaau aaauucauau aaccaaagu 720
ucgagcccaa acuggaagag uuccaggagg ugcaaagaug aaaagaauaa augaaaugau 780
aaaaggagcc gaauaaugca ugacuccaua uggaaccag gccaaaauau caaggauucu 840
augcgugguu uucgagagaa gacuagaaag auuagagcca uaaagaauau uuucaagugu 900
ggguaaaaca cgaacccaua uggguggacg ccagcguucu ggaauaaacc uacaagagua 960
aaauaaaauu gcccagguga ugauaacaau ggcaggaaaa aaaauuuggc guguaaaagg 1020
aacggucaac gcaauggcca aaagacaggc aaugccaaau uucccccaga auccaggaga 1080
uucaaugaca auacaagcaa aaaucaauu accugcuaga aacacauuu gcaaauugu 1140
ccaugaccau uucguauugc guagcaaacg aauguaggc auaggguuua agcuuguuuc 1200
caacuuguau uggaugcuc gguuacacgc agcaaggcgc uuuuuuaagg ucgaaagagc 1260
agacauugcu ucaaagaauu aucagaguaa aaaagggagc cguacgaaa aaauuucgua 1320
aggaauuaac cggaaaacua aaggaaaaaa aaggaauuuu uaugaaggaa agaaaguagc 1380
uauuaaauugc aagugucaag cacuaaaaag uagcgaugua aaauauuuua aaaaagaugg 1440
accgauuaac cauguucag cucacaguug ccagcaauca gggcuauuuu uuuaauuuuu 1500
uuauaaaauu gcuaauuaa uauaauuaa uuaguuuuuu aacuugcuuu uccucaaaaa 1560
accaauucga gaaaggaacu uuugcagagg caaaaaagcu u 1601

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(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Cys Phe Thr Ser Ser Tyr Phe Pro Asp Asp Arg Arg
5 10

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Cys Tyr Thr Ser Ile Glu Lys Tyr Asp Ile Ser Lys Ser Asp Pro
5 10 15

Leu Ala Ala Asp

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1553 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```

ttttacatat attattcacc caatatcata acaaaaacaa actgaatgat ggcattcttct 60
at ttgtgcgtt ccaaaaataat acaaaaaccg taccaattat tccactacta ttttcttctg 120
gagaaggctc ctggttctac agttagtgat ttgaattttg atacaaacat acaaacgagt 180
ttacgtaaat taaagcatca tcattggacg gtgggagaaa tattccatta tgggtttttg 240
gtttccatac tttttttcgt gtttgtgggt ttcccagctt cattttttat aaaattacca 300
ataatcttag catttgctac ttgtttttta atacctttaa catcacaatt ttttcttcct 360
gccttgcccg ttttcacttg gttggcatta tattttacgt gtgctaaaat acctcaagaa 420

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tggaaccag ctatcacagt taaagtttta ccagctatgg aaacaatttt gtacggcgat 480
aatttatcaa atgttttggc aaccatcact accggagtgt tagatatatt ggcattggta 540
ccatatggga ttattcattt cagtttccca tttgtacttg ctgctattat atttttattt 600
gggccaccga cggcattaag atcatttggg tttgcctttg gttatatgaa cttgcttggg 660
gtcttgattc aaatggcatt cccagctgct cctccatggg acaaaaaactt gcacggatta 720
gaaccagcta attattcaat gcacgggtct cctgggtggg ttggaaggat agataaattg 780
ttaggtgttg atatgtatac cacagggttt tccaattcat caatcatttt tggggcattc 840
ccatcgttac attcaggatg ttgtatcatg gaagtgttat ttttgtgttg gttgtttcca 900
cgattcaagt ttgtgtgggt tacatacgca tcttggcttt ggtggagcac gatgtatttg 960
acccatcact actttgtcga tttgattggg ggagccatgc tatctttgac tgtttttgaa 1020
ttcaccaaat ataaatattt gccaaaaaac aaagaaggcc ttttctgtcg ttggtcatac 1080
actgaaattg aaaaaatcga tatccaagag attgaccctt tatcatacaa ttatatccct 1140
gtcaacagca atgataatga aagcagattg tatacgagag tgtaccaaga gcctcagggt 1200
agtccccac agagagctga aacacctgaa gcatttgaga tgtcaaattt ttctagggtc 1260
agacaaagct caaagactca gggtccattg agtaatctta ctaacaatga tcaagtgcct 1320
ggaattaacg aagaggatga agaagaagaa ggcgatgaaa tttcgtcgag tactccttcg 1380
gtgtttgaag acgaaccaca gggtagcaca tatgctgcat cctcagctac atcagtagat 1440
gatttgatt ccaaagaaa ttagtaaaac agcagtttct attaatcttct ttatttcctc 1500
ctaattaatg attttatgtt caatacctac actatctgtt ttaatttcc tac 1553

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(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 472 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Met Ala Ser Ser Ile Leu Arg Ser Lys Ile Ile Gln Lys Pro

1

5

10

15

Tyr Gln Leu Phe His Tyr Tyr Phe Leu Leu Glu Lys Ala Pro Gly

60

	20	25	30
Ser Thr Val	Ser Asp Leu Asn Phe Asp Thr Asn Ile Gln Thr Ser		
	35	40	45
Leu Arg Lys Leu Lys His His His Trp Thr Val Gly Glu Ile Phe			
	50	55	60
His Tyr Gly Phe Leu Val Ser Ile Leu Phe Phe Val Phe Val Val			
	65	70	75
Phe Pro Ala Ser Phe Phe Ile Lys Leu Pro Ile Ile Leu Ala Phe			
	80	85	90
Ala Thr Cys Phe Leu Ile Pro Leu Thr Ser Gln Phe Phe Leu Pro			
	95	100	105
Ala Leu Pro Val Phe Thr Trp Leu Ala Leu Tyr Phe Thr Cys Ala			
	110	115	120
Lys Ile Pro Gln Glu Trp Lys Pro Ala Ile Thr Val Lys Val Leu			
	125	130	135
Pro Ala Met Glu Thr Ile Leu Tyr Gly Asp Asn Leu Ser Asn Val			
	140	145	150
Leu Ala Thr Ile Thr Thr Gly Val Leu Asp Ile Leu Ala Trp Leu			
	155	160	165
Pro Tyr Gly Ile Ile His Phe Ser Phe Pro Phe Val Leu Ala Ala			
	170	175	180
Ile Ile Phe Leu Phe Gly Pro Pro Thr Ala Leu Arg Ser Phe Gly			
	185	190	195
Phe Ala Phe Gly Tyr Met Asn Leu Leu Gly Val Leu Ile Gln Met			
	200	205	210
Ala Phe Pro Ala Ala Pro Pro Trp Tyr Lys Asn Leu His Gly Leu			
	215	220	225
Glu Pro Ala Asn Tyr Ser Met His Gly Ser Pro Gly Gly Leu Gly			
	230	235	240
Arg Ile Asp Lys Leu Leu Gly Val Asp Met Tyr Thr Thr Gly Phe			
	245	250	255
Ser Asn Ser Ser Ile Ile Phe Gly Ala Phe Pro Ser Leu His Ser			

260	265	270
Gly Cys Cys Ile Met Glu Val Leu Phe	Leu Cys Trp Leu Phe	Pro
275	280	285
Arg Phe Lys Phe Val Trp Val Thr Tyr	Ala Ser Trp Leu Trp	Trp
290	295	300
Ser Thr Met Tyr Leu Thr His His Tyr	Phe Val Asp Leu Ile	Gly
305	310	315
Gly Ala Met Leu Ser Leu Thr Val Phe	Glu Phe Thr Lys Tyr	Lys
320	325	330
Tyr Leu Pro Lys Asn Lys Glu Gly Leu	Phe Cys Arg Trp Ser	Tyr
335	340	345
Thr Glu Ile Glu Lys Ile Asp Ile Gln	Glu Ile Asp Pro Leu	Ser
350	355	360
Tyr Asn Tyr Ile Pro Val Asn Ser Asn	Asp Asn Glu Ser Arg	Leu
365	370	375
Tyr Thr Arg Val Tyr Gln Glu Pro Gln	Val Ser Pro Pro Gln	Arg
380	385	390
Ala Glu Thr Pro Glu Ala Phe Glu Met	Ser Asn Phe Ser Arg	Ser
395	400	405
Arg Gln Ser Ser Lys Thr Gln Val Pro	Leu Ser Asn Leu Thr	Asn
410	415	420
Asn Asp Gln Val Pro Gly Ile Asn Glu	Glu Asp Glu Glu Glu	Glu
425	430	435
Gly Asp Glu Ile Ser Ser Ser Thr Pro	Ser Val Phe Glu Asp	Glu
440	445	450
Pro Gln Gly Ser Thr Tyr Ala Ala Ser	Ser Ala Thr Ser Val	Asp
455	460	465
Asp Leu Asp Ser Lys Arg Asn		
470		

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Other nucleic acid (synthetic DNA)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

gactatttca ttatggggcc cc 22

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Other nucleic acid (synthetic DNA)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

gttaactcga gaaagtgcc atcagtgttc 30

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Other nucleic acid (synthetic DNA)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

gttaacggta cctcatcggt acaccgttc 29

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Other nucleic acid (synthetic DNA)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

gctaaacgac aatcctgac 19

- (2) INFORMATION FOR SEQ ID NO:41:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Other nucleic acid (synthetic DNA)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

cgttggccga ttcattaatg c 21

- (2) INFORMATION FOR SEQ ID NO:42:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 401 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Ala Asn Pro Phe Ser Arg Trp Phe Leu Ser Glu Arg Pro Pro

1

5

64

10

15

Asn Cys His Val	Ala Asp Leu Glu Thr	Ser Leu Asp Pro His Gln
20	25	30
Thr Leu Leu Lys Val	Gln Lys Tyr Lys Pro Ala Leu Ser Asp Trp	
35	40	45
Val His Tyr Ile Phe	Leu Gly Ser Ile Met Leu Phe Val Phe Ile	
50	55	60
Thr Asn Pro Ala Pro	Trp Ile Phe Lys Ile Leu Phe Tyr Cys Phe	
65	70	75
Leu Gly Thr Leu Phe	Ile Ile Pro Ala Thr Ser Gln Phe Phe Phe	
80	85	90
Asn Ala Leu Pro Ile	Leu Thr Trp Val Ala Leu Tyr Phe Thr Ser	
95	100	105
Ser Tyr Phe Pro Asp	Asp Arg Arg Pro Pro Ile Thr Val Lys Val	
110	115	120
Leu Pro Ala Val Glu	Thr Ile Leu Tyr Gly Asp Asn Leu Ser Asp	
125	130	135
Ile Leu Ala Thr Ser	Thr Asn Ser Phe Leu Asp Ile Leu Ala Trp	
140	145	150
Leu Pro Tyr Gly Leu	Phe His Phe Gly Ala Pro Phe Val Val Ala	
155	160	165
Ala Ile Leu Phe Val	Phe Gly Pro Pro Thr Val Leu Gln Gly Tyr	
170	175	180
Ala Phe Ala Phe Gly	Tyr Met Asn Leu Phe Gly Val Ile Met Gln	
185	190	195
Asn Val Phe Pro Ala	Ala Pro Pro Trp Tyr Lys Ile Leu Tyr Gly	
200	205	210
Leu Gln Ser Ala Asn	Tyr Asp Met His Gly Ser Pro Gly Gly Leu	
215	220	225
Ala Arg Ile Asp Lys	Leu Leu Gly Ile Asn Met Tyr Thr Thr Cys	
230	235	240
Phe Ser Asn Ser Ser	Val Ile Phe Gly Ala Phe Pro Ser Leu His	
245	250	255

Asn Cys His Val Ala Asp Leu Glu Thr Ser Leu Asp Pro His Gln		
	20	25 30
Thr Leu Leu Lys Val Gln Lys Tyr Lys Pro Ala Leu Ser Asp Trp		
	35	40 45
Val His Tyr Ile Phe Leu Gly Ser Ile Met Leu Phe Val Phe Ile		
	50	55 60
Thr Asn Pro Ala Pro Trp Ile Phe Lys Ile Leu Phe Tyr Cys Phe		
	65	70 75
Leu Gly Thr Leu Phe Ile Ile Pro Ala Thr Ser Gln Phe Phe Phe		
	80	85 90
Asn Ala Leu Pro Ile Leu Thr Trp Val Ala Leu Tyr Phe Thr Ser		
	95	100 105
Ser Tyr Phe Pro Asp Asp Arg Arg Pro Pro Ile Thr Val Lys Val		
	110	115 120
Leu Pro Ala Val Glu Thr Ile Leu Tyr Gly Asp Asn Leu Ser Asp		
	125	130 135
Ile Leu Ala Thr Ser Thr Asn Ser Phe Leu Asp Ile Leu Ala Trp		
	140	145 150
Leu Pro Tyr Gly Leu Phe His Tyr Gly Ala Pro Phe Val Val Ala		
	155	160 165
Ala Ile Leu Phe Val Phe Gly Pro Pro Thr Val Leu Gln Gly Tyr		
	170	175 180
Ala Phe Ala Phe Gly Tyr Met Asn Leu Phe Gly Val Ile Met Gln		
	185	190 195
Asn Val Phe Pro Ala Ala Pro Pro Trp Tyr Lys Ile Leu Tyr Gly		
	200	205 210
Leu Gln Ser Ala Asn Tyr Asp Met His Gly Ser Pro Gly Gly Leu		
	215	220 225
Ala Arg Ile Asp Lys Leu Leu Gly Ile Asn Met Tyr Thr Thr Cys		
	230	235 240
Phe Ser Asn Ser Ser Val Ile Phe Gly Ala Phe Pro Ser Leu His		
	245	250 255

Ser Gly Cys Ala Thr Met Glu Ala Leu Phe Phe Cys Tyr Cys Phe		
	260	265 270
Pro Lys Leu Lys Pro Leu Phe Ile Ala Tyr Val Cys Trp Leu Trp		
	275	280 285
Trp Ser Thr Met Tyr Leu Thr His His Tyr Phe Val Asp Leu Met		
	290	295 300
Ala Gly Ser Val Leu Ser Tyr Val Ile Phe Gln Tyr Thr Lys Tyr		
	305	310 315
Thr His Leu Pro Ile Val Asp Thr Ser Leu Phe Cys Arg Trp Ser		
	320	325 330
Tyr Thr Ser Ile Glu Lys Tyr Asp Ile Ser Lys Ser Asp Pro Leu		
	335	340 345
Ala Ala Asp Ser Asn Asp Ile Glu Ser Val Pro Leu Ser Asn Leu		
	350	355 360
Glu Leu Asp Phe Asp Leu Asn Met Thr Asp Glu Pro Ser Val Ser		
	365	370 375
Pro Ser Leu Phe Asp Gly Ser Thr Ser Val Ser Arg Ser Ser Ala		
	380	385 390
Thr Ser Ile Thr Ser Leu Gly Val Lys Arg Ala		
	395	400

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```

atggcaaacc ctttttcgag atggttttcta tcagagagac ctccaaactg ccatgtagcc    60
gatttagaaa caagtttaga tcccatcaa acgttggtga aggtgcaaaa atacaaaccc    120
68

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gctttaagcg actgggtgca ttacatcttc ttgggatcca tcatgctggt tgtgttcatt 180
actaatcccc caccttggat cttcaagatc cttttttatt gtttcttggg cactttattc 240
atcattccag ctacgtcaca gtttttcttc aatgccttgc ccatcctaac atgggtggcg 300
ctgtatttca cttcatcgta ctttccagat gaccgcaggc ctcctattac tgtcaaagtg 360
ttaccagcgg tggaaacaat tttatacggc gacaatttaa gtgatattct tgcaacatcg 420
acgaattcct ttttggacat tttagcatgg ttaccgtacg gactatttca ttttggggcc 480
ccatttgtcg ttgctgccat cttattcgta tttgggtccac caactgtttt gcaaggttat 540
gcttttgcatt ttgggttatat gaacctgttt ggtgttatca tgcaaaatgt ctttccagcc 600
gctcccccatt ggtataaaaat tctctatgga ttgcaatcag ccaactatga tatgcatggc 660
tcgcctgggtg gattagctag aattgataag ctactcggtg ttaatatgta tactacatgt 720
ttttcaaatt cctccgtcat tttcgggtgt tttccttcac tgcatcctgg gtgtgctact 780
atggaagccc tgtttttctg ttattgtttt ccaaaattga agcccttggt tattgcttat 840
gtttgctggt tatgggtggtc aactatgtat ctgacacacc attattttgt agaccttatg 900
gcaggttctg tgctgtcata cgttattttc cagtacacaa agtacacaca tttaccaatt 960
gtagatacat ctcttttttg cagatgggtca tacacttcaa ttgagaaata cgatatatca 1020
aagagtgatc cattgggtgc agattcaaac gatatcgaaa gtgtcccttt gtccaacttg 1080
gaacttgact ttgatcttaa tatgactgat gaaccagtg taagcccttc gttatttgat 1140
ggatctactt ctgtttctcg ttcgtccgcc acgtctataa cgtcactagg tgtaaagagg 1200
gcttaa 1206

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

atggcaaacc ctttttcgag atgggtttcta tcagagagac ctccaaactg ccatgtagcc 60
gatttagaaa caagtttaga tccccatcaa acgttggtga aggtgcaaaa atacaaaccc 120
gctttaagcg actgggtgca ttacatcttc ttgggatcca tcatgctggt tgtgttcatt 180

actaatcccg caccttggat cttcaagatc cttttttatt gtttcttggg cactttattc 240
 atcattccag ctacgtcaca gtttttcttc aatgccttgc ccatcctaac atgggtggcg 300
 ctgtatttca cttcatcgta ctttccagat gaccgcaggc ctcctattac tgtcaaagtg 360
 ttaccagcgg tggaaacaat tttatacggc gacaatttaa gtgatattct tgcaacatcg 420
 acgaattcct ttttggacat tttagcatgg ttaccgtacg gactatttca ttatggggcc 480
 ccatttgtcg ttgctgccat cttattcgta tttgggtccac caactgtttt gcaagggttat 540
 gcttttgcag ttgggttatat gaacctgttt ggtgttatca tgcaaaatgt ctttccagcc 600
 gctcccccag ggtataaaat tctctatgga ttgcaatcag ccaactatga tatgcatggc 660
 tcgcctgggtg gattagctag aattgataag ctactcggta ttaatatgta tactacatgt 720
 ttttcaaatt cctccgtcat tttcgggtgct tttccttcac tgcattccgg gtgtgctact 780
 atggaagccc tgtttttctg ttattgtttt ccaaaattga agcccttggt tattgcttat 840
 gtttgctggg tatgggtggc aactatgtat ctgacacacc attattttgt agaccttatg 900
 gcaggttctg tgctgtcata cgttattttt cagtacacaa agtacacaca tttaccaatt 960
 gtagatacat ctcttttttg cagatgggtca tacacttcaa ttgagaaata cgatatatca 1020
 aagagtgatc cattggctgc agattcaaac gatatcgaaa gtgtcccttt gtccaacttg 1080
 gaacttgact ttgatcttaa tatgactgat gaaccagtg taagcccttc gttatttgat 1140
 ggatctactt ctgtttctcg ttcgtccgcc acgtctataa cgtcactagg tgtaaagagg 1200
 gcttaa 1206

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

atggcaaacc ctttttcgag atggtttcta tcagagagac ctccaaactg ccatgtagcc 60
 gatttagaaa caagtttaga tccccatcaa acgttggtga aggtgcaaaa atacaaaccc 120
 gctttaagcg actgggtgca ttacatcttc ttgggatcca tcatgctgtt tgtgttcatt 180
 actaatcccg caccttggat cttcaagatc cttttttatt gtttcttggg cactttattc 240

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atcattccag ctacgtcaca gtttttcttc aatgccttgc ccatcctaac atgggtggcg 300
ctgtatttca cttcatcgta ctttccagat gaccgcaggc ctcctattac tgtcaaagtg 360
ttaccagcgg tggaaacaat ttatacggc gacaatttaa gtgatattct tgcaacatcg 420
acgaattcct ttttgacat tttagcatgg ttaccgtacg gactatttca ttatggggcc 480
ccatttgtcg ttgctgccat cttattcgta tttggtccac caactgtttt gcaaggttat 540
gcttttgcag ttggttatat gaacctgttt ggtgttatca tgcaaaatgt ctttccagcc 600
gtcccccat ggtataaaat tctctatgga ttgcaatcag ccaactatga tatgcatggc 660
tcgcctggtg gattagctag aattgataag ctactcggta ttaatatgta tactacagct 720
ttttcaaatt cctccgtcat tttcggtgct tttccttcac tgcattccgg gtgtgctact 780
atggaagccc tgtttttctg ttattgtttt ccaaaattga agcccttggt tattgcttat 840
gtttgctggt tatggtgggc aactatgtat ctgacacacc attattttgt agaccttatg 900
gcaggttctg tgctgtcata cgttattttc cagtacacaa agtacacaca tttaccaatt 960
gtagatacat ctcttttttg cagatgggtc tacacttcaa ttgagaaata cgatataatca 1020
aagagtgatc cattggctgc agattcaaac gatatcgaaa gtgtcccttt gtccaacttg 1080
gaacttgact ttgatcttaa tatgactgat gaaccagtg taagcccttc gttatttgat 1140
ggatctactt ctgtttctcg ttcgtccgcc acgtctataa cgtcactagg tgtaaagagg 1200
gcttaa 1206

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(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```

atggcaaacc ctttttcgag atggtttcta tcagagagac ctccaaactg ccatgtagcc 60
gatttagaaa caagtttaga tccccatcaa acgttggtga aggtgcaaaa atacaaaccc 120
gctttaagcg actgggtgca ttacatcttc ttgggatcca tcatgctgtt tgtgttcatt 180
actaatcccg caccttggat cttcaagatc cttttttatt gtttcttggg cactttattc 240
atcattccag ctacgtcaca gtttttcttc aatgccttgc ccatcctaac atgggtggcg 300

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ctgtatttca cttcatcgta ctttccagat gaccgcaggc ctcctattac tgtcaaagtg 360
ttaccagcgg tggaaacaat ttatacggc gacaatttaa gtgatattct tgcaacatcg 420
acgaattcct ttttggacat tttagcatgg ttaccgtacg gactatttca ttttggggcc 480
ccatttgtcg ttgctgccat cttattcgta tttgggtccac caactgtttt gcaagggttat 540
gcttttgcag ttgggttatat gaacctgttt ggtgttatca tgcaaaatgt ctttccagcc 600
gctcccccat ggtataaaaat tctctatgga ttgcaatcag ccaactatga tatgcatggc 660
tcgcctgggt gattagctag aattgataag ctactcggta ttaatatgta tactacagct 720
ttttcaaatt cctccgtcat tttcgggtgct tttccttcac tgcattccgg gtgtgctact 780
atggaagccc tgtttttctg ttattgtttt ccaaaattga agcccttggt tattgcttat 840
gtttgctggt tatggtgggt aactatgtat ctgacacacc attattttgt agaccttatg 900
gcaggttctg tgctgtcata cgttattttc cagtacacaa agtacacaca ttaccaatt 960
gtagatacat ctcttttttg cagatgggtca tacacttcaa ttgagaaata cgatatatca 1020
aagagtgatc cattgggtgc agattcaaac gatatcgaaa gtgtcccttt gtccaacttg 1080
gaacttgact ttgatcttaa tatgactgat gaaccagtg taagcccttc gttatttgat 1140
ggatctactt ctgtttctcg ttcgtccgcc acgtctataa cgtcactagg tgtaaagagg 1200
gcttaa 1206

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(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```

aatatgtata ctacatgttt ttcaaattcc 30

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(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Other nucleic acid (synthetic DNA)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

gttaactcga gaaagtgccc atcagtgttc 30

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Other nucleic acid (synthetic DNA)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

gttaacggta ccagaggaaa gaataacgc 29